

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number

TO: Mark Navarro Location: cm1/8A15

Art Unit: 1645

Monday, August 18, 2003

Case Serial Number: 09/904603

From: Barb O'Bryen

Location: Biotech-Chem Library

CM1-6A05

Phone: 308-4291

barbara.obryen@uspto.gov

Search Notes

O'Bryen, Barbara

From:

Sent: To:

Subject:

Navarro, Albert

Wednesday, August 06, 2003 4:23 PM

O'Bryen, Barbara 09/904.603

Mark Navarro 1645 306-3225 8A15

Hello Barb,

Could I trouble you for a search and an interference search of:

SEQ ID NO: 1-2

Thanks

Mark

2/24/97



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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Voluntary Nesults Feedback Form
➤ I am an examiner in Workgroup: Example: 1610
Relevant prior art found, search results used as follows:
☐ 102 rejection
☐ 103 rejection
☐ Cited as being of interest.
Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
Foreign Patent(s)
 Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
> Relevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
☐ Results were not useful in determining patentability or understanding the invention.
Comments:

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                                      Homo sapiens
                                                                                                                       Homo sapiens, MAP1 light chain IMAGE:3909192, mRNA, complete
                                                   Homo sapiens (human)
                                                                                          BC015810.1
                                                                                                           BC015810
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PVLDKTKELVPDHVNMSELVKIIRRRLQLNPTQAFFLLVNQHSMVSVSTPIADIYEQE
KDEDGFLYMVYASQETFGF"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               through the I.M.A.G.E. Consortium/II.NI. at: http://image.ilui.dov
Series: IRAK Plate: 15 kow: e Golumo: 15
This clone was selected for full length sequencing herause if
passed the following selection criteria: matched mRNA di: 142195
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Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jett Stott
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-rimail.nih.gov
Tissue Procurement: ATCC
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Contact: MGC help desk
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                                                                                                                                                                                                                                                                              GCACCCCAGCAAAATCCCGGTGATCATCGAGCGCTACAAGGGTGAGAAGCAGCTGCCGT
                                                                                                                    CCTGGACAAGACCAAGTTTTTGG1CCCGGACCATGTCAACATGAGCGAGTTGGTCAAGAT
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315 c 276 q
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/protein_id-"AAH15810.1"
/db_xref-"G1:16041839"
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/mol_type="mkNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MPSDRPFKQRRSFADRCKEVQQIRDQHPSKIPVIIEHYKGEKQL
PVLDKTKFLVPDHVNMSELVKIIKRRLQLNPTQAFFLLVNQHSMVSVSIPIAUIYEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Uterus, le
/clone_lib="NIH_MGC_71"
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                                                                                                                                                                                                                                                                                                              Submitted (10-JUL-2002) GSF, Institut fuer Bioinformatik MIPS, Ingolstaedter Landstr. 1, 85764 Neuherberg, Germany Clone from S. Wiemann, Molecular Balaysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                912 bp mRNA
Homo sapiens mRNA; cDNA DKFZp761L0515 (f
complete cds.
AL833855
AL833855.1 GI:21739336
                                                                                                                                                                                                                            German Genome Project.
This clone (DKFZp761C515) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 912)
Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           /gene="DKFZp761L0515"
66. .431
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/tissue_type="amygdala"
/clone_lib="761 (synonym:
DH10B; sites NotI + SalI"
                    /gene="DKFZp761L0515"
/note="bA346K17.1 (Rattus norvegicus)"
/codon_start=1
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/db_xref="taxon:9606"
/chromosome="20"
      /product="hypothetical protein"
                                                                                                /dev_stage="adult"
                                                                                                                        hamy2).
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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Klausner,R.D., Collins,F.S., Wagner,L., Shem Altschul,S.F., Zeeberg,B., Buetow,K.H., Schau
                                                                                                                                     984 bp
Mus musculus RIKEN cDNA 4922501H04
IMAGE:3256801), complete cds.
BC010506
                                                       Mammalia;
                                                                   Eukaryota;
                                                                             Mus musculus
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                                      mmalia; Eutheria; (bases 1 to 984)
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Metazoa;

Chordata; Rodentia; mouse)

Craniata; Vertebrata; | Sciurognathi; Muridae;

Euteleostomi;
; Murinae; Mus

Shenmen, C.M., Schaefer, C.F., Shenmen, C

Schuler, G

Ö

Derge, J.G.,

GI:14714881

mRNA gene, mRNA

linear

(CDNA

clone

ROD 16-APR-2003 clone MGC:6325

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135 GCGCGATGCCCTCAGACCGGCCTTTCAAGCAGCGGCGGAGCTTCGCCGACCGCTGTAAGG
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               GCATGTGCCCCCCTAGTCAGAGGGCA 640
                                                       CCTGCCCAGAGAGCTTCTGGTTCCTGAACTGAGCTGCCTCTACCGTGGTGGGCTGGCCAG
                                                                                                                                                                                                                                        AGGTACAGCAGATCCGCGACCAGCACCCCGCAAAATCCCGGTGATCATCGAGCGCTACA
GCATGTG-CCCCCTAGTCAGAGGGCA
                                                                                                                                    TCGGCTTCTGAGCCAGCAGTAGGGGGGGCTCGGCCTGGGAGTCGGGGGGCCCCGGTCAGGC
                                                                                                                                                                                             ACGAGCAGGAGAAAGACGACGACGACGCTTCCCTCTATATGGTCTACGCCCTCCCAGGAAACCT
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PVLDKTKFLVPDHVNMSELVKIIRRRLQLNPTQAFFLLVNQHSMVSVSTPIADIYEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAD38714.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium on the Consortium of the Consortium o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 6 Row: g Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseqed, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: Lothar Hennighausen Ph.D., ph.D.
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analysis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host-"DH10B"
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                                                                                                                                                                                                                                                                                                                                       /gene="4922501H04Rik"
                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV-SPORT6"
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                                  Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                            Homo sapieus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens microtubule-associated protein 1 light chain
                                                                     Phelan, M. and Farmer, A
                                                                                                Koundinya, M., Raphael, J., Moreira, D.,
                                                                                                                                          Kalnine, N., Chen, X., Rolfs, A., Halleck, A.,
                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordatu; Cianiata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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FEATURES

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PRI 13-MAY-2003

Kelley, T.,

Hines, L.,

LaBaer, J., Lin, Y.,

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421 CACCCATCGCTGACATCTATGAACAGGAGAAGGATGAAGACGGATTCCTCTACATGGTCT
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                                                   ACCGTGGTGGGCTGGGCAGGCATGTGCCCCCC 627
                                                                                                                                                              GGGGGGCCCCGGTCAGGCCCTGCCCAGAGAGAGCTTCTGGTTCCTGAACTGAGCTGCC1C-1 595
                                                                                                                                                                                                                                                 ACGCCTCCCAGGAAACCTTCGGCTTCTGAGCCAGCAGTAGGGGGGCTCGGCCTGGGATTC 5-6
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TCCCCAGTGGATTAGGCAGAGATGTGACACCC
                                                                                                           TGGGAGTTCTGGTCAGGTTCTCCCCAGGGAGGTCCTGGCTCCTAAACTAAGCTA1110AG
                                                                                                                                                                                                                    ACGCCTCCCAAGAAACCTTCGGCTTCTGAGTCAAGAGGAGGGGAG------GGGGGTTGC
                                                                                                                                                                                                                                                                                                                                                       CGCCCATCGCGGACATCTACGAGCAGGAGGAGAAAGACGAGGACGGCTTCCTCTATA1GGTCT
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This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission Submitted (13-MAY-2003) BD Biosciences Clontech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 366)

Kalnine, N., Chen, X., Rolfs, A.,
Koundinya, M., Raphael, J., Morei
Phelan, M. and Farmer, A.
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                                                                                                                  CTGCTGGTGAACCAGCACAGCATGGTGAGTGTGTCCACGCCCATCGCGGACATCTACGAG
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                                                            CAGGAGAAAGACGAGGACGGCTTCCTCTATATGGTCTACGCCTCCCAGGAAACCTTCGGC
                                                                                       CAGGAGAAAGACGAGGACGGCTTCCTCTATATGGTCTACGCCTCCCAGGAAACCTTCGGC
                                                                                                                                                                                                                                                                                                                                                AGCGAGTTGGTCAAGATCATCCGGCGCCGCCCTGCAGCTGAACCCCCACGCAGGCCTTCTTC
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PVLDKTKFLVPDHVNMSELVKIIRRRLQLNPTQAFFLLVNQHSMVSVSTPIADIYEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAP36120.1"
/db_xref="GI:30583743"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="microtubule-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
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SOURCE
    ORGANISM
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                                                                                                                       Human DNA sequence from clone RP11-346K17 on chromosome 20 Conta: a novel gene encoding a protein similar to the cell division control protein 91 (CDC91) from Yeast, a novel gene encoding two isoforms similar to MAPIALC3 (micotubule-associated proteins 1A, lightchain 3) from Rat, 3 CpG islands, ESTs, STSs and GSSs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stuart, J., Lincoln, S.E., Altus, C.M., Dufour, G., Chalup, M., Hillman, J.L., Jones, A.L., Yu, J.Y., Wright, R.J., Gietzen, D., Yap, P., Dahl, C.R., Momiyama, M.G., Bradley, D., Rohatgi, S., Harris, B., Roseberry, Ann, M., Gerstin, E.H., Peralta, C.H., David, M.H., Panzer, Scott, R., Flores, V., Daffo, A., Marwaha, R.Chen, A.J., Chang, S.C., Au, A.P. and Inman, R.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secretory molecules
Patent: WO 02020756-A 76 14-MAR-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
                      Homo
                                                              AL118520.26
                                                                                                          complete sequence.
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AX740487
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGGCGCCGCCTGCAGCTGAACCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAACTGAGCTGCCTCTACCGTGGGTGGGCCTGGGCATGTGTGCCCCCCTAGTCAGAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTCGGCCTGGGAGTCGGGGGGCCCCGGTCAGGCCCCTGCCCAGAGAGCTCCTGGTTCCT
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sapiens
                                            CDC91; CpG island;
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="rtaxon:9606"
/note="Incyte ID No: LG:247776.14:2000SEP08"
/note="Incyte ID No: LG:347776.14:2000SEP08"
1 318 c 354 g 183 t 2 others
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                      (human)
                                                              GI:9801544
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99.3%;
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Pred. No. 2e
                                                                                                                                                                                                                                       157975 bp
                                          microtubule-associated proteins
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W002020756
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                misc_feature
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                            misc_feature
                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chr20
Rp11-346K17 is from the library RPCI-11.2 constructed at the Rp11-346K17 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-346K17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP1-346K17 is at 1 in this sequence. The true right end of clone RP5-1181N3 is at 157876 in this sequence. The true right end of clone RP5-1181N3 is at 157876 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requests: clonerequest@sanger.ac.uk
on Aug 14, 2000 this sequence version replaced q1:9717213.
During sequence assembly data is compared from overlapping clones
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CH10 1SA, UK. E-mail enquiries: humquery:sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variation annotation may not be found in the sequence submission
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l (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     feature key.
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                                                                                                                                                                                                                                                     2964. .1524/
/gene="ba346K17.1"
join(2964. .2991,5980. .6104,15283. .15338,15422. .15528,
join(2964. .2991,5980. .6104,15283. .15338,15422. .15528,
15811. .16247)
/gene="ba346K17.1"
/product="ba346K17.1.1 (Novel protein similar to MAPIALC3
/micoribule-associated proteins la/IB light chain 3) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA
/db_xref="taxon:9606"
/chromosome="20"
/clone="RP11-346K17"
                         /note="match: GSS: Em:AQ834732"
complement(5177. .5581)
                                                                             /note="THEIC repeat: matches 1.
complement(5105, .5567)
                                                                                                                                                                                                          /note="MLT1J repeat: matches 120..292 of consensus" 2964..16247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                           Em:AW161970 Em:AA016389 Em:AA197682 Em:AW161293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RPCI-11.2"
19. .630
                                                                                                                                       /evidence=not_experimental
3543. .3896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: GSS: Em:AQ541128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                    complement(join(16618. .17054,31179. .31321,37624. ...
41512. .41655,44528. .44682,72117. .72214,96690. .907
93951. .94060,100239. .100301,101350. .101409,113255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: GSS: Em:AQ186762"
10052. .10443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="I,1ME2 repeat: matches 6044.
complement(9544. .10055)
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7334. .7542
                                                                                                                                                                                                                  /product="bA346K17.2 (A novel protein similar to the cell
division control protein 91 (CDC91, YLR459W or 1912z.2)
                                                                                                                                                                                                                                                                                                                                                                                          /gene="bA346K17.2"
complement"
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VYASQETFGF″
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (micotubule-associated proteins
Rat, isoform 2)"
/protein_id="CAC14079.1"
/db_xref="GI:10944273"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"match: proteins: Sw:P87068 Sw:Q62625 Tr:Q9SL04
Tr:Q94272 Sw:Q41515"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: GSS: Em:AQ246853" 10102. .10183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"match: GSS: Em:AQ141567"
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YEQEKDEDGFLYMVYASQETFGF"
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/db_xref="GI:10944272"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="DA346K17.1.1 (Novel protein similar to MAPPALC3 (micotubule-associated proteins lA/18 light chain 3) from Rat, isoform 1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
/product="bA346K17.1.1 (No
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/note="match: proteins: Tr:094272 Tr:09SL04
Tr:09SLN6 Sw:009490 Sw:062625 Sw:041515"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"MER66A repeat: matches 27. .438 of consensus"
join(6053. .6104,15283. .15338,15422. .15528,158il.
                                                                                complement(16618
                                                                                                  control protein 91 (CDC91,
/evidence=not_experimental
                                                                                                                                                                                           from Yeast)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="34 copies 2 mer cc 66% conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKARAMPSDRPFKORRSFADRCKEVQQ1kDQHPSK1PV11EkYKGEKQLPVLDK1KFI
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join(<14797. .14983,15283.
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                                                 /qene="bA346K17
                                                                                                                                                              /note="A novel protein similar to the cell division
                                                                                                                                                                                                                                                                            133031. .133160))
/gene="bA346K17.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="ELPPAAAAAVLSASPGALEREARSPRSPQ1ADISPRPRAPACAP
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                                                                                                                                    YLR459W or L9122.2)
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                                                                                                                                                          GGCTCGGCCTGGGAGTCGGGGGGCCCCGGTCAGGCCCTGCCCAGAGAGCGTTCTGGTTCCT
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/db_xref="GI:10944274"
/db_xref="GI:10944274"
/translation="MAAPLVLVLVVAVTVRAALFRSSLAEFISERVEVVSPLSSWKRV
/translation="MAAPLVLVLVAVTVRAALFRSLAEFISERVEVVSPLSSWKRV
VESLSLLDLGVSPYSGAVEHERPLITYLFFELDVAELVFMITDALTAIALYFAIQDF
NKVVFKKQKLLLELDQVAPDVAELIRTPMEMRYIPLKVALFYLLNPYTILSCVAKSTC
AINNTLIAFFILTIKSSAFLSAIFLALATYQSLYPLTLFVPGLLYLLQRQYIPVKMK
SKAFMIESWEYAMMYVGSLVVIICLSFFLLSSWDFIPAYVGFLSVPDLTPNIGLFWY
FFAEMFEHFSLFVCVPQINVFFYTIPLAIKLKEHPIFFMFTQIAVTAIFKSYFTVGD
VALYMAFFPVWNHLYRFLRNIFVLTCIIIVCSLLFPVLMHLWIYAGSANSNFFYAITL
TENVGQILLISDYFYAFLRREYYLTHGLYLTAKDGTEAMLVLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="54 copies 2 23863. .23908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="22 copies 2
22079 .22186
                                                                                                                                                                                                                                                                                                                                                                                                            /note="34 copies 2
29295. .29742
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/gene="bA346K17.2"
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/evidence-not_experimental
/product='bA346kI7.2 (A novel protein similar to the cell
/product='bA346kI7.2 (A novel protein yuka59w or L9122.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: ESTs: Em:AI315824 Em:AW753001 Em:AW046539 Em:AA317421 Em:AA157236 Em:AW354502 match: proteins: Sw:P41733"
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41512. .41655,44528. .44682,72117. .72214,90690. .9079
93951. .94060,100239. .100301,101350. .101409,113255.
133031. .133160))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="26 copies 2 mer ac 88% complement(21837. .22058)
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 HTG; H'
Rattus
                         AC116062 
AC116062.6 GI:30578911
                                                unordered pieces.
                                                            Rattus norvegicus
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            HTGS_PHASE1;
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9

norvegicus

HTGS_DRAFT; (Norway rat

HTGS_FULLTOP

clone

66877 bp DI CH230-76N21,

DNA 21, WORKING

linear

HTG

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SEQUENCE,

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100 CCCCAGAGCCCCGGCCTGCGCGCGCGCGCGCGCGCGCGCTCAGACCGGCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (10-APR-2000) Institute of
No. 220 Handan Road, Shanghai 200433,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus MAPIA/1B light chain AF255953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                   CTTCCTCTATATGGTCTACGCCTCCCAGGAAACCTTCGG 498
                                                                                                                                          CCGGCGCCTGCAGCTGAACCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGAGAG
                                                                                                                                                                                                                                                                                                                                     CAAGCAGCGGGGGAGCTTCGCCGACCGCTGTAAGGAGGTACAGCAGATCCGCGACCAGCA 219
CTTCCTGTACATGGTTTATGCCTCGCAGGAGACATTCGG 434
                                                             CATGGTGAGTGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAGAAAGACGAGGACGACGG
                                                                                                                          CAGACGGCGCTTGCAGCTCAATGCTAACCAAGCCTTCTTCCTCCTGGTGAATGGGCACAG
                                                                                                                                                                                      CCCCACCAGATCCCAGTGATTATAGAGCGATACAAGGGGGAGAAGCAGCTGCCGTCCT
                                                                                                                                                                                                                                                                     CCCCAGCAAAATCCCGGTGATCATCGAGCGCTACAAGGGTGAGAAGCAGCTGCCCTCCT
                                                                                                                                                                                                                                                                                                                CAAGCAGCGCCGGAGCTTTGAACAAAGAGTGGAAGATGTCCGGCTCATCCGGGAGCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MPSEKTFKORRSFEORVEDVRLIREOHPTKIPVIIERYKGEKQL
PVLDKTKFLVPDHVNMSELIKIIRRLOLNANQAFFLLVNGHSMVSVSTPISEVYESE
RDEDGFLYMVYASQETFGTAMAV"
260 c 256 g 208 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="MAP1A/1B light chain 3 subunit"
/protein_id="AAL83723.1"
/db_xref="GI:19070137"
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Direct Submission

Submitted (13-MAY 2003) Human Genome Sequencing Center, Deposit of Molecular and Human Genetics, Baylor College of Medicine of Molecular and Human Genetics, Baylor College of Medicine Baylor plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced qi:24942360. The sequence in this assembly is a combination of BAC based and whole genome shotqun sequencing reads assembled using A (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each conting decrease of the property of the
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Submitted (24-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morqan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,
Morqan,M., Norris,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
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,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
,Cuiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
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table shotgun sequence only conties will be indicated in the teature genome shotgun sequence reads. Both end sequences and whole genome may extend beyond the ends of the clone and there may be sequence contigs within a contig-scalfold that consist entirely of whole by sized gaps filled with Ns to the estimated size. The sequence assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated

* NOTE: Estimated insert size may differ from sequence length * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) * NOTE: This is a 'working draft' sequence. It currently Consensus quality: 54966 bases at least Q40 Consensus quality: 58172 bases at least Q20 Consensus quality: 60570 bases at least Q20 Estimated insert size: 39548; sum-of-contigs estimation Quality coverage: 8x in Q20 bases; sum-of-contigs estimation Center project name: GMCW Center clone name: GH230-76N21 web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help:bcm.tmc.edu Center: Baylor Assembly program: Atlas 3.0; Center ----- Genome Center code: BCM Summary Statistics Project Information College of Medicine

NOTE: ITLS IS a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary came between the continuous. arbitrary. Gaps between the contigs are represented as

as soon as it is available and the accession number will

be updated with the finished sequence

runs of N, but the exact sizes of the gaps are unknown

This record will

be preserved 21411 21511 23020 23120 24272 24372 $\frac{13863}{13963}$ 10074 11268 11368 18181 18281 19888 16298 15079 15179 12463 19988 16398 6978 7078 8547 8647 9974 5814 5914 1214 1314 2355 2455 3486 3586 2141 2151 15178: 16297: 16397: 18180: 18280: 19887: 19987: 1126 1136 1396 1507 1007 contig gap of contig gap of unknown contiq of 1152 contiq of 1509 gap of unknown contiq gap of contiq contig gap of contig gap of gap of contig gap of contig gap of contiq gap of contig gap of contig contiq of 1213 of 1116 t unknown of 1119 f unknown
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                                                                                                             AGCAGCGGCGAGCTTCGCCGACCGCTGTAAGGAGGTACAGCAGATCCGCGACCAGCACC
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Roya, A., Santos, R., Schauer, S., Schupback, R., Scaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Young, R., Wilson, B., Wu, X., Wyman, D., Ye, M. J., Young, G., Valel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M. J., Young, G., Vale, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M. J., Young, G., Vale, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M. J., Young, G., Vale, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M. J., Young, G., Vale, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M. J., Young, G., Vale, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M. J., Young, G., Vale, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Vale, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Vale, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Vale, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Vale, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Vale, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Wall, R., Vo, A., Whan, D., Ye, W. J., Young, G., Whan, Y., Whan, D., Ye, W. J., Young, G., Whan, Y., Whan, D., Ye, W. J., Young, G., Whan, Y., Whan, D., Ye, W. J., Young, G., Whan, Y., Whan, D., Ye, W. J., Young, G., Whan, Y., Whan, D., Ye, W. J., Young, G., Whan, Y., Whan, Y., Whan, Y., Whan, Y., Whan, Y., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 6 (bases 1 to 190843)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Faro,S., Ferreira,P., Graham.I., Grand-Pierre,N., Hagos,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stoljanovic, N., Talamas, J
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Vial R., Vola Wilson R., Wilson R., Vonna, G., Zainou, J.,
Vonna, G., Zainou, J.,
Vial R., Vola Wilson R., Waman, D., Vonna, G., Zainou, J.,
Vial R., Van Wilson R., Waman, D., Vonna, G., Zainou, J.,
Vial R., Van Wilson R., Waman, D., Vonna, G., Zainou, J.,
Vial R., Van Wilson R., Waman, D., Vonna, G., Zainou, J.,
Vial R., Van Wilson R., Waman, D., Vonna, G., Zainou, J.,
Vial R., Van Waman, D., Vonna, G., Zainou, J.,
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Vial R., Van Waman, D., Vonna, G., Zainou, J.,
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Vial R., Van Waman, D., Vonna, G., Zainou, J.,
Vial R., Van Waman, D., Vonna, G., Zainou, J.,
Vial R., Van Waman, D., Vonna, G., Zainou, J.,
Van Waman, D., Vonna, G., Zainou, J.,
Vial R., Van Waman, D., Vonna, G., Zainou, J.,
Van Waman, D., Vonna, G., Zain
                                       Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:19745075. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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AC103943.3
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Mus muscullus (house mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA linear HTG 21-AUG-2002 WORKING DRAFT SEQUENCE, 6 ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cook, A.
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ORIGIN
                                                                                                                                                                                                                                               BASE COUNT
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                                                                                                                                    Query Match
Best Local Similarity
Matches 299; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
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                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 3076 soontig of 3076 bp in length

* 3077 3176; gap of 100 bp

* 32406 soontig of 29229 bp in length

* 32506 65653; contig of 33148 bp in length

* 65654 65753; gap of 100 bp

* 65754 119294; contig of 33541 bp in length

* 119295 119394; gap of 100 bp
                                            CAAGCAGCGGCGGAGCTTCGCCGACCGCTGTAAGGAGGTACAGCAGATCCGCGACCAGCA 219
                                                                                        CCCCAGAGCCCCGGCCTGCGCGCCCAGCCGGGGCCCGGCGATGCCCTCAGACCGGCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                 54525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             provided by the submittor
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119395
163109
163209
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Insert size: 190343; sum-of-contigs
Quality coverage: 11.4 in Q20 bases; agarose-fp
Quality coverage: 12.6 in Q20 bases; sum-of-contigs
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Consensus quality: 189833 bases at least Q40 consensus quality: 190117 bases at least Q30 Consensus quality: 190281 bases at least Q20
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Center clone name: 460_I_18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
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119395. .163108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref-"taxon:10090"
/clone="RP23-460I18"
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163209. .190843
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Sequence 1714 from Patent
AX402038
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                            GATTATAGAGGGATACAAGGGTGAGAAGCAGCTGCCGGTCCTGGACAAGACCAAG11CCT
                                                                                                         GATCAICGAGCGCTACAAGGGTGAGAAGACAGCTGCCGGTCCTGGACAAGACACAAGILLII
                                                                                                                                               CTTCCTGTACATGGTTTATGCCTCGCAGGAGACATTCGG
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                                        {\tt TGTACCTGATCACGTGAATATGAGCGAACTCATCAAGATAATTAGAAGGCGCCTGCAGCT}
                                                                 GGTCCCGGACCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGGCGCCGCCTGCAGCT
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 norvegicus
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                                                                                                                                                                                                                                                                                                                                                    /mol_type="qenomic DNA"
/db_xref="taxon:10116"
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76.6%;
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Pred. No. 1.7e
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LOCATION/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; ;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                     TGCCTCCCAGGAGACGTTCGG
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                                                                                     GCCCATCGCGGACATCTACGAGCAGGAGAAAAGACGAGGACGGCTTCCTCTATATGGTCTA
                                                                                                                              GAACCCCACGCAGGCCTTCTTCCTGCTGCTGAACCAGCACAGCATGGTGAGTGTGTCCAC
                                                                                                                                                                     GGTCCCGGACCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGGCGCGCCGCCTGCAGCT
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a 255 c 213 g
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/db_xref="taxon:10116"
/note="Light chain 3 subunit
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Pred. No. 1.7e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (28-JAN-1994) James A. Hammarb
Submitted (28-JAN-1994) James A. Hammarb
Anatomy, Bowman Gray School of Medicine,
Winston-Salem, NC 27157_1010, USA
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Molecular characterization of light c
subunit of MAPIA and MAPIB
J. Biol. Chem. 269 (15), 11492-11497
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/product="light chain 3 su
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/protein_id="AAA20645.1"
/db_xref="GI:455109"
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Search Job tin	Db	Qy	Вb
Search completed: August 15, 2003, 08:56:26 Job time : 2460 secs	365 TGCCTCCCAGGAGACGTTCGG 385	478 CGCCTCCCAGGAAACCTTCGG 498	+05 ACCCATCTCTGAAGTGTACGAGAGCGAGAGAGATGAAGACGGCTTCCTGTACATGGTCTA 364

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Result
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Copyright (c) 1993 - 2003 Compugen Ltd.
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nucleotide sequence.		Probe #892 used to Human liver single	#926	bone mari	Probe #885 for den	foeta	Human secreted pro Human breast cell	DNA encoding novel	Oligonacleotide to	Oligonacheotide to			Probe #21696 ased Human liver single		Human brain extres	Human Cytoskeleton	Human MPLs encodin	bear .	Human tumour suppr				Human Secretory po	dation solutions that		Human bone marrow	Human brain expres	

RESULT 1 AAV43780 ID AAV43780 standard; cDNA; 642 HP. XX AC AAV43780; AC AAV43780; AC AAV43780; DI 20-NOV-1998 (first entry) XX DE Human microtubule associated protein hLC3 XX ss; human; microtubule-associated protein: XX Cancer. XX Homo sapiens. XX Location/Qualifiers FT CDS /*tau-a FT CDS /*tau-a FT /product-ahlc: XX PN WO9837197-A1. XX PP 23-FEB-1998. XX PF 23-FEB-1998. XX PR 24-FEB-1997; 97US-0805117. XX PR 24-FEB-1997; 97US-0805117. XX PR 24-FEB-1997; 97US-0805117. XX CINCY-) INCYTE PHARM INC. XX Coli SK, Hillman JL;

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ABQ54481

ABQ54481 standard;

cDNA;

1000

ВP

wore: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/puh/nuh/ichca

directly

of the printed

ftp.wipo.int/pub/published_pct_sequences

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CC ABP4328) and to cDNAs encoding them (ABQ54131-ABQ5305), and also ce encompasses polypeptides 90% identical and polypucleotides 95% identical cto the sequences of the invention. The invention additionally relates to cenominant vectors and host cells comprising human ovarian antigen polypucleotides against human ovarian ovarian antigen cc of ovarian antigen polypucleotides and polypeptides in diagnosing, cc treating, prognosing or preventing various ovary and/or breast cancer, and cdisorders. Such conditions include ovarian cancer and breast cancer, and cdisorders. Such conditions include ovarian cancer and breast cancer, and cdisorders. Such conditions include ovarian cancer and breast cancer, and cdisorders. Infections (e.g., infertility, disorders of pregnancy, anovulation, cc disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitus, oophoritis and cvapinitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus crythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, candurate ovarian antigen expression or activity. The polynucleotides may also be used in screening for compounds which conformation of individuals and in forensic analysis, and the cuseful in disease diagnosis, drug targeting and phenotyping. The present cuseful in disease diagnosis, drug targeting and phenotyping. The present curvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
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DB; ABP41404.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID No
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                                                                                           cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymuosteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                     diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
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                                                                                                                                                                                                                                                                            secreted protein; fusion protein; gene therapy; protein therapy;
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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the acue to a human immunoglobulin Fc portion (e.g. AAX20403) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 83 novel genes and their fragments (nucleic acid sequences AAX00415-X2049; unino acid sequences AX00415-X2049; unino acid sequences AX00415-X2049; unino acid sequences AX0027) which are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the new polypocleonides. Specific uses are described for each of the 86 not would take a sample or by determining the presence of mutations in the new polypocleonides. Specific uses are described for each of the 86 not would be a sample or by determining the presence of mutations in the new polypocleonides. Specific uses are described for each of the 86 not would be a sample or by determining the presence of mutations in the new polypocleonides. Specific uses are described for each of the 86 not would be a sample or which there are the second of the 86 not would be a sample or which there are the second of the 86 not would be a sample or which there are the second of the 86 not would be a sample or which there are the second of the 86 not would be a sample or which there are the second of the second
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S-0054215.
S-0054217.
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polynucleotides, based on which tissues (see AAX20412 for described uses). they are most highly expresse

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                                                                                                      Conservative
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99.5%;
                                                                                                             Score 627; DB 20;
Pred. No. 1.8e-126;
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                                                                                   New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutal responsible for genetic disorders or other traits and to assubiodiversity
                                     Claim 1; SEQ ID No 9784; 103pp; English
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23-AUG-2000;
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DB; ABG09793.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polymcleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
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                               476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTCCCGCAGCCGCAGCCGCCGTGCTCAGCGCGAGCCCCGGAGCCCCTTGAGCGCGAGGCGC
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CCGA-CCGCTGTAAGGAGGTACAGCAGATCCG-CGACCAGCACCCCGAGCAAAATCCCGGT
                                                                                                                                                                                                                                                                                                                                             CGCCCAGCCGGGCCCGCGCGATGCCCTCAGACCGGCCTTTCAAGCAGCGGCGGAGCTTCG
                                                                                                                                                                                                                                                                                                                                                                                                    GGAG-CCCCGGAGCCCCAAACCGCAGACACATCCCCGCGCCCCAGAGCCCCGGCCTGCG
                                                         ACGCCCATCGCGGACATCTACGAGCAGGAGAAAGACGAGGACGGCTTCCTCTATATGGTC
                                                                                                                                                                         TGGTCCCGGACCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGGCGCCGCCTGCAGC
                                                                                                                                                                                       TGGTCCCGGACCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGGCGCCGCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCCGCAGCCGCAGCCGCGTGCTCAGCGCGAGCCCCGGAGCCCTTGAGCGCGAGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              704 BP; 131 A; 263 C; 191 G; 119
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Pred. No. 1.3e-89;
""" matches 1;
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Human brain Expressed Sequence

Tag

EST01371

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Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enriched oligonucleotides and corresp. sequences - used markers for human genes transcribed in-vivo, facilitate % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       most human genes
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AGTA
                                                                                                                                                                                                                                                                 AGATCATCCGGCGCCCGCAGCTGAACCCCACGCAGGCCTTCTTCCTGCTGGTGAACC
                                                                                                                                                                                                                                                                                                                                                                                   CCGTCCTGGACAAGACCAAGTTTTTGGTCCCGGACCATGTCAACATGAGCGAGTTGGTCA
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                                                                                                                                                                             AGCACAGCATGGTGAGTGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAGAAAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCTTTCAAGNAGCGGCGGA-NTTCGCCGACCGCTGTAAGGAGGTACAGCAGATCCGCG
                                       AGTA 515
                                                                                                             AGGACGGCTTCCTCTATATGGTCTACGCCTCCCAGGAAACCTTCGGC-TTCTGAGCCAGC
                                                                                                                                                                                                                                                                                                                                                            CCGTCCTGGACAAGACCAAGTTTTTGGTCCCGGACCATGTCAACATGAGCNAGTTGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCAGCACCCCAGCAAAATCCCGGTGATCATCGAGCGCTACAAGGGTGAGAAGCAGCTGC
                                                                                        AGGACGGCTTCCTCTATATGGTCTACGGCTCCCAGGAAACCTTCGGCTTTCTGAGNCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mapping; locations; chromosomes; chromosomal; ss
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97.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
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Pred. No. 1.8e-62;
0; Mismatches 8
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 $\begin{array}{l} \forall \, \mathsf{X} \, \mathsf{X} \, \mathsf{X} \, \mathsf{X} \, \mathsf{X} \, \mathsf{Y} \, \mathsf{X} \, \mathsf{T} \, \mathsf{X} \, \mathsf{T} \, \mathsf{X} \, \mathsf{Y} \, \mathsf{Y}$

QY DЬ QΥ Вb Ş ₽ Š

Ϋ́O В δλ Db 40 рь

Polynucleotide sequences encoding human secretory proteins useful gene therapy of e.g. genetic deficiency disorders, cancers, and diseases caused by intracellular parasites -

Jones

Yu JY,

Dahl CR;

R, EH,

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05-SEP-2000

05-SEP-2000

05-SEP-2000

05-SEP-2000

05-SEP-2000

06-SEP-2000

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07-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      meningitis; abscess; prion diseases; cerebral palsy; neuroskeletal disorder; peripheral nervous system disorder; dermatomyositis; polymyositis; myopathy; myasthenia gravis; mental disorder; lourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; gene; secretory protein; secretory polynucleotides; SFIM: SPIM-related disease; somatic gene therapy; germline gene therapy; severe combined immunodeficiency; intracellular parasite protection:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     motor neuron disorder; demyellnating disease; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secretory polynucleotide (sptm)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungal parasite; protozoan parasite: cell proliferative disorder; cancer; numune disorder; AIDS; neurological disorder; Parkinson's disease;
                                                                                                                                                  INCYTE GENOMICS
                                                                                                                          Lincoln SE,
                                                                                                                                                                                                                                                                                                                                    ; 2000US-230518P.
; 2000US-230519P.
; 2000US-230595P.
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2000US-230896P.
2000US-230897P.
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2000US-230864P.
2000US-230865P.
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2000US-230515P.
2000US-230517P.
                                                                             incoln SE, Altus (M. Dufour GE, Chalup MS, Hi
'u JY, Wright RJ, Gletzen D, Liu TF, Yap PE,
Bradley DL, Rohatqi SD, Harris B, Roseberry
Peralta CH, David MH, Panzer SR, Flores V, D
Chen AJ, Chang SC, Au AP, Inman RR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US27297
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2000US-231163P
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2000US-230989P
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2000US-230597P
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                                                                                                                           Hillman JL;
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AAS73981
AC AAS7
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AX DT 13-|
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Best Local
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  31-MAR-2000;
                                                   30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                        DNA encoding
                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS73981 standard; cDNA; 794 BP
                                                                                                                                                            WO200175067-A2
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                                                                                                                                                                                                                                                                                          chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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  2000US-0540217
                                                                                                                                                                                                                                                                                                                                     novel human diagnostic protein #9785
                                                                                                                                                                                                                                                                                  mapping; gene mapping; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 A; 318 C; 354 G;
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99.3%;
                                                                                                                                                                                                                                                          imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No. 2.8
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2;
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                                                                                                                                                                                                                                                                                     forensic;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, compolymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in a disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in a consisting for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and campostics, gene mapping, identification of mutations are sequences. AAS64197-AAS94564 represent novel human are sequences of the invention.

Consisting the sequence of the invention of mutations in the printed among the products are sequenced to the sequence of the invention of mutations in the printed of the printed and products are sequenced to a product of the printed and products are sequenced to a printed and products of the printed and products are present in the printed and products are present of the printed and printed and pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
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                                                     ftp.wipo.int/pub/published_pct_sequences.
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Sequence 794 BP; 151 A; 253 C; 231 G; 159 T; 0 other;

Query Match Best Local :

Local Similarity

45.6%; 91.6%;

Length

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                                                 CTGAGCC-AGCAGTAGGGGGGCTCGGCCT-GGGAGTCGGGGGGGCCCCGGTCAGGCCCT-G
                                                                                       AAGAC-GAGGACGGCTTCCT-CTATATGGTCTACGCCTCCC---AGGAAACCTTCGGCTT
                          CCCAGAGAGCTTCTGGTTCCTGAA-----
                                                                                                                             TCCGCGACCAGCACCCCAGCAAAATCCCCGGTGATCATCGAGCGCTACAAGGGTGAGAAGC
              CCCAGAGAGCTCCTGGGTCTGGAAACTTGGAGCCTGGCCTCTTAACCCGTGGTGGGCTGG
                                                                                                                                                                                                         AGCTGCCCGTCCTGGACAAGACCAAGTTTTTGGTCCCGGACCATGTCAACATGAGCGAGT
                                                                                                                                                                                                                  AGCTGCCCGTCCTGGACAAGACCAAGTTTTTGGTCCCGGACCATGTCAACATGAGCGAGT
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Pred. No. 4.9e-54;
0; Mismatches 20;
                                -CTGAGCTGCCTCTACCGTGGTGGGCTGG
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Best Local
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human
                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                printed specification, but was obtained in electronic
from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                fetal liver. The present sequence probe of the invention.
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26-MAY-2000;
                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                 genome-derived single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     foetal liver single
                                                                                                                                                                                        Similarity
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                                                                                                                                                   CCGGCGCCGCCTGCAGCCTGAACCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCACAG
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                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                   CTTCCTCTATATGGTCTACGCCTCCCAGGAAACCTTCGGCTTCTGAGCCAGCAGTAGGGG
                                               CTTCCTCTATATGGTCTACGCCTCCCAGGAAACCTTCGGCTTCTGAGCCAGCAGTAGGGG
                                                                                            CATGGTGAGTGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAGAAAAGACGAGGACGA
                                                                                                                             CAGGCGCCCTGCAGCTGAACCCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCACAG
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                                                                                CATGGTGAGTGTGCCACGCCCATCGCGGACATCTACGAGCAGGAGAAAGACGAGGACGG
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gene expression
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                                                                                                                                                                            Conservative
                                                                                                                                                                                                                          BP;
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2000US-0236359.
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2000US-0632366
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                                                                                                                                                                                      39.9%;
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                                                                                                                                                                          Score 255.2; DB 2
Pred. No. 4.3e-46;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                                                                                                                                                                                                                                                                                                                                               sequence listing;
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                                                                                                                                                                                                                                                                                                                                                                                       fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                acid probes
                                                                                                                                                                                                 DB 22;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human probes which are derived from the sequence expression in brain cell samples brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophronia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                          Single
                                                                                                                                                                                                                                                                                                                                 Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon;
microarray; Alzheimer's disea
                                                                                                                                                           Sequence
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257; Conserv
                                                                                                                                                                                                                                                                                          exon
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CATGGTGAGTGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAGAAAGACGAGGAGGACGG
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                  CTTCCTCTATATGGTCTACGCCTCCCAGGAAACCTTCGGCTTCTGAGCCAGCAGIAGGG
                                               standard;
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                                                                                                                                                                                                                                                                                                                                                                     2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                    Conservative
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                                                                                                                                                           HP;
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                                                                                                                             39.98;
98.88;
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                                                                                                                                                                                                                                                            650pp · Sequence Listing;
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O: Mismatches
                                                                                                                             Score 255.2:
Pred. No. 4.
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se; multiple sclerosis; s
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                                                                                                                                                          102 T:
                                                                                                                 . 4.3e-46;
. 1.3e-3;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                          Example 4;
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                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing
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27-SEP-2000;
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                                                                                                                                                                                      al Similarity
257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        genome-derived single exon nucleic acid probes useful
zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                         570
                                                                  CCGGCGCCTGCAGCTGAACCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCACAG
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                                                  CATGGTGAGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAGAAAGACGAGGACGG
                                                                                                                   CAGGCGCCGCCTGCAGCTGAACCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCACAG
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Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:
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                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
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                                                                                                                                                                                                                                                     97 A; 158 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DK,
                                                                                                                                                                                                                                                                                          invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed
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                                                                                                                                                                                                    39.9%;
                                                                                                                                                                                                                                                                                                                                                                                                       9809; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w,
                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single exon
                                                                                                                                                                                                      Score 255.2;
Prèd. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon; gene expression
                                                                                                                                                                                                                                                       213 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphoma; myeloma; ss
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR
                                                                                                                                                                                    4.3e-46;
.ches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analysis; probe;
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                                                                                                                                                                                    0;
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ID AAI40
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Best Local :
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                     Sequence 570
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genetic disorder; ;
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                                                                                                                                                                                                                                                                                                                                                                                          analyzing
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30-JUN-2000;
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                                                                                                                                                                         257;
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                                                                                                                                                                                                                                                                                                                                                                                         genome-derived single exon nucleic acid zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
CTTCCTCTATATGGTCTACGCCTCCCAGGAAACCTTCGGCTTCTGAGCCAGCAGTAGGGG
                                                                CATGGTGAGTGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAGAAAGACGACGAGGACGACGG
                                                                                                                              CCGGCGCCTGCAGCTGAACCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCAGAG
                                                CATGGTGAGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAGAAAGACGAGGACGG
                                                                                                              CAGGCGCCGCCTGCAGCTGAACCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCACAG
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                                                                                                                                                                                                                                                                                                                                                               SEQ
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                               IJ
                                                                                                                                                                                                                                     97 A; 158 C;
                                                                                                                                                                                                                                                                                                                                                            No 9653; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                   39.9%;
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                                                                                                                                                                        Score 255.2;
Pred. No. 4.3e
0; Mismatches
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                                                                                                                                                                                                                                     213 G; 102 T; 0 other;
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No. 4.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                           probes
                                                                                                                                                                         Indels
                                                                                                                                                                                                     Length
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ABS34996
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Query Match
Best Local Similarity
Matches 257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                    The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS$501-ABS$5005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver - \,
                                                                                                                                                                                                                                                                                                                                                WPI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
26-MAY-2000;
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                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coronary heart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
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                                                                              WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liver single exon probe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single exon nucleic acid probe; liver; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                           SEQ ID No 9986; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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  Conservative
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                                                                           ftp.wipo.int/pub/published_pct_sequences
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2000US-0236359.
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2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease;
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                                                   A; 158
            39.9%;
98.8%;
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            Score 255.2; DB 2
Pred. No. 4.3e-46;
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  Mismatches
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                                                    102 T;
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                       DB 23;
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Gaps
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cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preterably the hepatotoxicity of a compound, comprising detecting the level of

expression in a tissue or cell sample exposed to the

TWO OF

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ABK63807
                                                                                                                                                                                                                                                                                                               06-JUN-2001;
13-JUN-2001;
19-JUN-2001;
09-JUL-2001;
The invention relates to methods for predicting toxic effects of compounds or the progression of these taxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to wome expression in unexposed tissues or
                                                                                                                       effects by determining the changes
cells exposed to the toxin and compunexposed tissues or cells -
                                                                                                                                                     Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues of
                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                        02-NOV-2000;
11-MAY-2001;
                                                                                        Claim
                                                                                                                                                                                                                                                Mendrick
                                                                                                                                                                                                                                                                                (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-2001;
22-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat sequence differentially expressed in response to a hepatotexin #1714
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                                                                                    1; Seq ID No 1714; 239pp; English
                                                                                                                                                                                                                                                                                GENE
                                                                                                                                                                                                                                              D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCCTCTATATGGTCTACGCCTCCCAGGAAACCTTCGGCTTCTGAGCCAGCAGTAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATGGTGAGTGTCCACGCCCAICGCGGACATCTACGAGCAGGAGAAAGACGACGACGACGACGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hepatotoxin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTCGGCCTGGGAGTCGGGCGGGCCCCGGTCAGGCCCTGCCCAGAGAGCTCCTGGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCCTCTATATGGTCTACGCCTCCCAGGAAACCTTCGGCTTCTGAGCCAGCAGTAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATGGTGAGTGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAGAAAGACGAGGAGAGGAGGA
                                                                                                                                                                                                                                                                                                               2001US-290645P.
2001US-292336P.
2001US-295798P.
2001US-297457P.
2001US-298884P.
2001US-303459P.
                                                                                                                                                                                                                                                                                LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                              Porter
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2001US-290029P
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                                                                                                                                                                                                                                                MK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  centrilobular necrosis;
                                                                                                                                                                                                                                              Johnson KR,
                                                                                                                          and comparing these to gene ex-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ę
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                                                                                                                                                                                                                                              Castile
                                                                                                                                                                                                                                              AI.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  steatosis
                                                                                                                                                                                                                                              Elashoff Mr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug screening;
                                                                                                                                         expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4'91)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    519
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CC the genes listed in the specification, where differential expression of CC the genes is indicative of at least one toxic effect or progression. CC The method can also be used to identify an agent which modulates the CC toxic response and predict cellular pathways that a compound modulates (CC in a cell. The methods utilise a set of at least two probes (on a solid CC support in kit form), where each of the probes comprises a sequence that CC system comprising a database containing information identifying the CC expression level in a tissue or cell sample exposed to a hepatotoxin of a CC identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a CC identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a CC identifying the expression level in a tissue or cell for at least one gene CC isted in the specification. The method is useful for elucidating global CC changes in gene expression and for identifying toxicity markers in CC toxicity markers in drug screening and toxicity markers in CC toxicity markers in drug screening and toxicity assays. The genes and CC gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell considered to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present CC which is differentially expressed in response to a hepatotoxic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 292
                                                                  Human; ss; go
SPTM-related
                                           severe combined
                                                                                                                                 Human
                                                                                                                                                                             03-OCT-2002
                                                                                                                                                                                                                                                                   ABL99776 standard; cDNA; 1910
                      fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 861 BP; 215 A; 255 C; 213 G; 178 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              365
                                                                                                                                                                                                                                                                                                                                                                                                                       478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                 secretory
  parasite;
disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                            TGCCTCCCAGGAGACGTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCATCGGGGACATCTACGAGCAGGAGAAAAGACGAGGACGGCTTCCTCTATATGGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAACCCCACGCAGGCCTTCTTCCTGCTGCAGCAGCAGCACAGCATGGTGAGTGTGTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCCTCCCAGGAAACCTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTACCTGATCACGTGAATATGAGCGAACTCATCAAGATAATTAGAAGGCGCCTGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCCCGGACCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGGCGCCGCCTGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAACAAAGAGTGGAAGATGTCCGGCTCATCCGGGAGCAGCACCCCACCAAGATCCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCCGACCGCTGTAAGGAGGTACAGCAGATCCGCGACCAGCACCCCAGCAAAATCCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCCATCTCTGAAGTGTACGAGAGCGAGAGAGATGAAGACGGCTTCCTGTACATGGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAATGCTAACCAAGCCTTCTTCCTCCTGGTGAATGGGCACAGCATGGTGAGTGTCTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGAGCCAGGACCCCCGCGCCCATGCCGTCCGAGAAGACCTTCAAACAGCGCCGGAGCTT
                                                                                      gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                        (first entry)
                                                                  disease;
           secretory protein; secretory polynucleotides; SPTM; sease; somatic gene therapy; germline gene therapy; immunodeficiency; intracellular parasite protection; protozoan parasite; cell proliferative disorder; cancer;
                                                                                                                                 polynucleotide
protozoan parasite;
AIDS; neurological c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.3%;
76.6%;
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); Mismatches
                                                                                                                                                                                                                                                                 ВР
                                                                                                                             (sptm)
                                                                                                                                                                                                                                                                                                                                                                            385
disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238.6;
                                                                                                                               31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24;
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06-SEP-2000

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06-SEP-2000

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06-SEP-2000

07-SEP-2000

07-SEP-2000
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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05-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   motor neuron disorder; demyelinating disease; multip
meningitis; abscess; prion diseases; cerebral palsy;
neuroskeletal disorder; peripheral nervous system di
dermatomyositis; polymyositis; myopathy; myasthenia
mental disorder; Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                    06-SEP-2000;
06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000;
06-SEP-2000;
                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS
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05-SEP-2000;
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2000US-230988P
2000US-230999P
2000US-230990P
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2000US-230864P.
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2000US-230597P.
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2000US-230517P.
2000US-230518P.
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2000US-230514P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sclerosis;
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Marwaha Momiyama MG, Jones ΑĽ, EH, ĭu Lincoln SE, Bradley DL, Rohatqi SD, Harris B, Roseberry Peralta CH, David MH, Panzer SR, Flores V, D Chen AJ, Chang SC, Au AP, Inman RR Hillman JL; AM; Dahl CR;

P-PSDB; 2002-315658/35)B; ABB97779.

Ş 밁 Qy ₽

Claim 1; Page 268-269; 585pp; English.

The invention comprises the amino acid and coding sequences of human secretory (SPTM) proteins. The SPTM DNA and amino acid sequences are useful for treating a disease or condition associated with the expression of functional SPTM. The SPTM DNA sequences are useful for somatic or germline gene therapy to correct a genetic deficiency (e.g. severe combined immunodeficiency). The SPTM DNA sequences are also useful in providing protection against intracellular parasites (e.g. fungal parasites and protozoan parasites). The SPTM DNA and protein sequences are also useful for diagnosing cell proliferative disorders, cancer, immune disorders (e.g. AIDS), neurological disorders (e.g. Parkinson's disease), motor neuron disorders, demyelinating diseases (e.g. multiple colarons). sclerosis), meningitis, abscesses, prion diseases, peripheral nervous system cerebral palsy,

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RESULT 15
AAI58816
ID AAI588
XX AAI588
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XX AAI58
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XX Human
XX Human
XX Anny
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 273;
                                                                                                                  21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                 03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dermatomyositis and polymyositis, myopathy, myasthenia gravis, a disorders (e.g. Tourette's syndrome). cDNA sequences ABL99746 - represent human secretory polynucleotides of the invention.
                                                                                                                                                                                                                                          26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            chemokinetic;
                           29-NOV
                                                                                                                                                                                                                                                                                            26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI58816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAGGAGGTACAGCAGATCCGCGAGCAGCACCAGCAAAATCCCGGTGATCATCGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGITCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCTACGAGCAGGAGAAAGACGAGGACGGCTTCCTCTATATGGTCTACGCCTCCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTCAACATGAGCTCATCAAGATAATTAGAAGCCGCTTACAGCTCAATGCTAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCCGCGATGCCCTCAGACCGGCCTTTCAAGCAGCGGCGGAGCTTCGCCGACCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1910 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGTATGAGAGTGAGAAAGATGAAGATGGATTCCTGTACATGGTCTATGCCTCCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCTTCTTCCTGTTGGTGAACGGACACAGCATGGTCAGCGTCTCCACACCAATCTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome, other uses include the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 20
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                                                                                                 CCTTCTTCCTGTTGGTGAACGGACACACCATGGTCAGCGTCTCCACACCAATCTCAAAG
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RESULT 1

US-08-805-117-2 US-08-805-117-2 ; Patent No. Sequence GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L. APPLICANT: Goli, Surya K. TITLE OF INVENTION: NOVEL MICRETUBULE-ASSOCIATED PROTEIN NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEO for Windows Version CURRENT APPLICATION DATA: TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: IMMEDIATE SOURCE: FILING DATE: ATTORNEY/AGENT INFORMATION: STREET: 3174 POR CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94304 CLONE: NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: 1:F APPLICATION NUMBER: FILING DATE: Herew LIBRARY: THYRNOT03 CLONE: 1441378 TOPOLOGY: TYPE: TELEX: STRANDEDNESS: single LENGTH: ADDRESSEE: 2, Application US/08805117 5, 5955312 nucleic acid 640 base pairs 3174 Porter Drive Incyte Pharmaceuticals, inear Herewith US/08/805,117 FF-0211 US

Query Match Best Local Similarity

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Score 640; DB 2; Pred. No. 1.9e-134; ; Mismatches 0;

Length 640; ; Indels

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Matches 640;

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RESULT 2
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OPERATING SYSTEM: DOS
SONTWARE: FASTSEO for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,838
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/805,117
                                                                                                                                                                                                                                                                                                              Sequence 2, Application Patent No. 6280733
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL MICROTUBULE-ASSOCIATED
NUMBER OF SEQUENCES: 3
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                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
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US-09-199-838-2
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Best Local s
Matches 640
Sequence 707, Application Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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                                                                                                                                                                                                 CTCCCAGGAAACCTTCGGCTTCTGAGCCAGCAGTAGGGGGGCTCGGCCTGGGAGTCGGGG
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                                                                            GGTGGGCTGGGCAGGCATGTGCCCCCCTAGTCAGAGGGCA
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Pred. No. 1.9e-134;
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; LOCATION: (109)..(486)
US-09-620-312D-707
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Best Local
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SOFTWARE: pt_Ft_genes Version 1.0
SEQ ID NO 707
LENGTH: 768
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APPLICANT: Tang, Y.
APPLICANT: Liu, Ch
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APPLICANT:
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TITLE OF INVENTION: NO. 6569662el
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-21
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APPLICANT:
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TYPE: DNA
ORGANISM: Homo sapiens
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Local Similarity 74.1%;
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: Liu, Chenghua
:-undi, Vinod
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                                                                                                                       TGTATGAGAGTGAGAAGATGAAGATGGATTCCTGTACATGGTCTATGCCTCCCAGGAGA
                                                                                                                                    TCTACGAGCAGGAGAAAGACGAGGACGGCTTCCTCTATATGGTCTACGCCTCCCAGGAAA 491
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Zhang, Jie
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John Tillinghast
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Wang, Zhiwei
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Chen, Rui-hong
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Pred. No. 1.5e-39;
0; Mismatches 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 768.
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; ORGANISM: Human
US-09-708-725A-3
                                                                                                                                                                                                          ; GENERAL INFORMATION:
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Best Local .
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             TITLE OF INVENTION: USES THERE F
TILE REFERENCE: CLOON842
CURRENT APPLICATION NUMBER: US/09/708,725A
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/244.428
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEO ID NOS: 4
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CL000842
CURRENT APPLICATION NUMBER: US/09/708,725A
                                                                                                                                                                                          APPLICANT: LADUNGA et al
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al Similarity 68.5%;
296; Conservation
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FastSEQ for Windows Version
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pred. No. 2.5e-39;
0; Mismatches 136;
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Sequence 4937, Applicatio
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION: NUCC
TITLE OF INVENTION: NUCC
TITLE OF INVENTION: AER
FILE REFERENCE: 107196.
CURRENT APPLICATION NUMBER
CURRENT FILING DATE: 199
PRIOR APPLICATION NUMBER
PRIOR APPLICATION NUMBER
PRIOR APPLICATION NUMBER
PRIOR FILING DATE: 1998
PRIOR FILING DATE: 1998
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 4937
LENGTH: 939
TYPE: DAM
OGRANISM: Pseudomonas au
US-09-252-991A-4937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; EILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: US 60/074 70^
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Best Local
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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LENGTH: 201
TYPE: DNA
ORGANISM: Human
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                     TGGTCCCGGACCATGTCAACATGAGCGAGGTTGGTCAAGATCATCCGGCCCCGCCTGCAGC
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                                                                                             TGATCATCGAGCGCTACAAGGGTGAGAAGCAGCTGCCCGTCCTGGACAAGACCAAGTTTT
                                                                                                                                                     TCGCCGACCGCTGTAAGGAGGTACAGCAGATCCGCGACCAGCAGCACCCCAGCAAAATCCCGG
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TGGAGCAGGCCACGGAGCGCAACGGCGAGCGCCCGCCTGGCCCTGCACCGCCTCGGCC
                                                                                                                                                                                          AGGCGATCCGCCAGGGCATGGCGCTGTTCGACGACCTCAAGCACCACCCGCGCATCCGCA 131
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                                                              TGCTCACCGAGGAACTCGACGCCAGCATCCAGATGCACGTCCACGAGACCGCCTTCGAGG
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45.3%;
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74.78;
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Pred. No. 0.0017;
0; Mismatches 234;
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Pred. No. 7.6
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US-09-252-991A-4950
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LENGTH: 1317
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARBGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-27

RUMBER: OF SEQ ID NOS: 33142
848
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                                                               788
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                               ACGCCTCC
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                                                                                             CGCCCATCGCGGACATCTACGAGCAGGAGGAAAGACGAGGACGGCTTCCTCTATATGGTCT
                                                                                                                                                                                                                                                                           TGATCATCGAGCGCTACAAGGGTGAGAAGCAGCTGCCCGTCCTGGACAAGACCAAGTTTT
GCGGCTTC
                                                             TGCTGGTGGAAACCAACAGCTCGGTGATCCACTGCCCGGAATCCAACCTCAAGCTGGCCA
                                                                                                                            TGCTCGGCCCACGCTTCCAGGCGGTGCACATGACCCAGGTGGACGACGACGACCTGGCGA
                                                                                                                                                        TGAACCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCACAGCATGGTGAGTGTCTCCA
                                                                                                                                                                                          TGGAGCAGGCCACGGAGCGCAACGGCGAGCGCCCGCCTGGCCCTGCACCGCCTCGGCC
                                                                                                                                                                                                            TGGTCCCGGACCATGTCAACATGAGCGAGGTTGGTCAAGATCATCCGGCGCCGCCCTGCAGC
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855
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45.3%;
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Pred. No. 0.0018;
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RESULT 8

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOST:
TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOST:
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-77
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
SEQ ID NO 4998
LENGTH: 1932
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                                                                                                                                                                                                                                                                                 RESULT 9
US-09-252-991A-1709
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                                                                                                                                                                                                                                        Sequence 1709, Application US/09252991A Patent No. 6551795
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107
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ORGANISM: Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTCGGCCCACGCTTCCAGGCGGTGCACATGACCCAGGTGGACGACGACGACCTGGCGA
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                                                                                                                               C J. Rubenfield et al.
ION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
ION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136

    J. Rubenfield et al.
    ION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
    107196.136

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Pred. No. 0.
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RESULT 10 US-09-620-312D-597

; Sequence 597, Application US/09620312D
; Patent No. 6569662

GENERAL INFORMATION:

Tang,

Chenghija Tom Vinod

APPLICANT:

APPLICANT:
APPLICANT:

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Zhao, Qing A. Wehrman, Tom Ren, Feiyan Chen, Rui-hong Asundi, Vir Zhang, Jie

APPLICANT: APPLICANT:

Wang, Jian-kui Zhou, Pinq Ma, Yunqinq

Yang, Yonghong Xue, Aidong J

APPLICANT APPLICANT: APPLICANT:

Wang, Dunrui Wang, Zhiwei John Tillinghast

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SEQ ID NO 1709
LENGTH: 1764
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Pseudomonas
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 1221
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CIGCGCGCAGAIC 1233
                         CTGCCCAGAGAGC 568
                                                      CGACCTCACTCCGGCCAGCCTGGAGCCGCTGGGGGTGAAGGTCTACGAGCTGAGCGAATC
                                                                                CGGCTTCTGAGCCAGCAGTAGGGGGGCTCGGCCTGGGAGTCGGGGGGGCCCGGGTAAGGCC
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US-09-702-705-78
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; LOCATION: (282)..(635)
US-09-620-312D-597
SOFTWARE: Fas
SEQ ID NO 78
SEQ TH: 519
                                                                                                                                                                                                                                                                                APPLICANT: Wang, T
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SEQ ID NO 597
LENGTH: 2038
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT:
                                                                                                                                                                                                                                                                                                              Sequence 78, Application US/09702705 Patent No. 6504010
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Best Local 9
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 165;
                                                CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
                                                                                              TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C14
                                                                                                                                                                                                  APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/620,312D CURRENT FILING DATE: 2000-07-19 PRIOR APPLICATION NUMBER: 09/552,317 PRIOR ETILING DATE: 2000-04-25 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. 6569662el Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
                                                                                                                                                     APPLICANT:
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                                                                                                                                                               Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
                                    FastSEQ for Windows Version 3.0
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Lodes, Michael A.
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DS: 1105
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Pred. No.
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; SOFTWARE: FastSEQ for I
; SEQ ID NO 78
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-78
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                                                                                                                                                                                       Query Match 7.4%;
Best Local Similarity 47.9%;
Matches 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 78, Application US/09736457 Patent No. 6509448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
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                                                                                                                                                      122 CCCAGCCGGGCCCGCGCGATGCCCTCAGACCGGCCTTTCAAGCAGCGGCGGAGCTTCGCC
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                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 3.0
                ATCGAGCGCTACAAGGGTGAGAAGCAGCTGCCCGTCCTGGACAAGACCAAGTTTTTGGTC
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AAGCGCCTGCGCAAGGAGGCAAGGAGGCGCCCCCATGGAGAAGCCGGAAGTGGTGAAG
                                                                                           GACCGCTGTAAGGAGGTACAGCAGATCCGCGACCAGCACCCCAGCAAAATCCCGGTGATC
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Retter, Marc
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Lodes, Michael
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Bangur, Chaitanya
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47.98;
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Pred. No. 0.041;
0; Mismatches 148;
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US-08-911-853-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                           hes 203; Conservative
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                                                             ATCGAGCGCTACAAGGGTGAGAAGCAGCTGCCCGTCCTGGACAAGACCAAGTTTTTGGTC
                                                                                             CGCCTACGCCACACGCCAAGAGCCTGGCCGAGACCCTGGGCGACATCTCCGAGGGG
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VENTION: EXPRESSION SYSTEM
VENTION: EXPRESSION LEVELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM
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APPLICANT: Quax, Wilhelmus J
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 52.
                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                             NAME: Glaister, Deb
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
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                                          GCCAACCIGGCCCGCICGCIGGACATCCCCAGCACCCCTICGGCCAATGCGCGGIAATI
                                                                      CCCAGCCGGGCCCGCGATGCCCTCAGACGGGCTTTCAAGCAGCGGCGGAAGCTICTC
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RESULT 15

US-09-479-453-14

US-09-479-453-14

Sequence 14, Application US/09479453

Patent NO. 6313283

GENERAL IMFORMATION:
APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J.

TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: APPRESSION LEVELS

TITLE OF SEQUENCES: 37
                                        Qγ
       В
                                                                                                                                                    ; STRANDEDNESS: si; TOPOLOGY: linear US-09-479-453-14
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                                                                                           Query Match
Best Local Similarity
                                                                                Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOSTMANDE: PERTESO FOR USER
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1950 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,453
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 920
CITY: Palo Alto
STATE: CA
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ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                 64 GCCCCGGAGCCCCAAACCGCAGACACATCCCCGGGCCCCAGAGGCCCGGGCCTGCGC--G 121
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1126 CGCGGCGCACCGGCGGCCTCGGCG 1150	1126	Δb
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1066 ATCGTGGAAATCTCCGGGGGACATCAGCGACGCCCTCGGCGTGCAGTGGGCGGTGGATGCC 112:	1066	ф
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946 CGCGCCGACGAGGCCTCAATGCCCTGGTCCTGCTGGCCGATCCGGGACACCGTGGCGACC 100	946	Дb
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886 TTGAAGACCGCGGAGGGTGGTGGCGAAGCCGCCAGCAAGCCGCAGAACATCCTGATC 945	886	Ъ
242 ATCGAGCGCTACAAGGGTGAGAAGCAGCTGCCCGTCCTGGACAAGACCAAGTTTTTTGGTC 301	242	QΥ
826 CGCCTACGCCACAGCGCCAAGAGCCTGGCCGAGACCCCTGGGCGACATCTCCGAGGGG 885	826	В
182 GACCGCTGTAAGGAAGGTACAGCAGAATCCGCGACCAGCAACCCCAGCAAAATCCCGGTGATC 241	182	QУ
766 GCCAACCTGGCTCGCTGGACATCCCCAGCACCCGTTCGGCCAATGCGCGGGTAATT 825	. 766	дb
122 CCCAGCCGGGCCCGCGCGATGCCCTCAGACCGGCCTTTCAAGCAGCGGCGGAGCTTCGCC 181	122	Qy

Search completed: August 15, 2003, 09:32:03 Job time: 76 secs

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Result
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2: /cgn2_6/ptodata/2/pna/U
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4: /cgn2_6/ptodata/2/pna/U
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen
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Sequence 26, Appl
Sequence 1019, App
Sequence 1019, App
Sequence 4591, App
Sequence 4591, App
Sequence 2841, App
Sequence 873, App
Sequence 7205, App
Sequence 26616, App
Sequence 20079, A
Sequence 52126, Ap
Sequence 52126, Ap
Sequence 2792, Ap
Sequence 2792, Ap
Sequence 2792, Ap
Sequence 2792, App
Sequence 2792, App
Sequence 275, App
Sequence 275, App
Sequence 277, App
Sequence 1485, App
Sequence 173, App
Sequence 193, App
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		98206 Secr Secr	tion US/0 al. al. 12p1 NUMBER:	449-26 26, Applica 100, Applica 111: Ruben Exter 111: Rub	SULT 1 -09-820-649-26 Sequence 26, Application Sequence 27, Application Sequence 10, Application Sequence 10, Application APPLICANT: Ruben et al. TITLE OF INVENTION: 83 FILE REFERENCE: PZ012P1 CURRENT APPLICATION NUM CURRENT ETILING DATE: 2	ESULT 1 S-09-820-649- Sequence 26, Sequence 26, APPLICANT: TITLE OF IN FILE REFERE CURRENT APP
		ALIGNMENTS				
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	x	-80 8	1205		40.8	44
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1205,	s	6 US-1	3804		41.4	42
X	v.	6 US-10	3804		41.4	41
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1141.	S	6 08-1	2433	5.5	42.2	35
1141,	S	6 US-1	2433			34
830,	cs.	6 US-1	2433		42.2	ω U
4714,	w	6 US-1	2410			32
	S.	6 US-1	2410		•	31
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US-09-820-649-26
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LENGTH: 1014
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Best Local :
                                                                                                                      Matches
                                                                                                                                                                                                                                                    Remaining Prior Application data
NUMBER OF SEQ ID NOS: 353
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/054,246
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,215
PRIOR FILING DATE: 1997-07-30
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/054,214 FILING DATE: 1997-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/054,218 FILING DATE: 1997-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/054,234 FILING DATE: 1997-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-07-30
APPLICATION NUMBER: 60/054,209
FILING DATE: 1997-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US98/15949 FILING DATE: 1998-07-29 APPLICATION NUMBER: 60/054,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: 1999-01-26
                              239
    273
                                                                                                                   tch 71.9%: al Similarity 99.8%; 461; Conservative
US/09/236,557
                                                                                                                 Score 460.4; DB 5;
Pred. No. 2.9e-104;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                removed - See File Wrapper or
                                                                                                                                               Length 1014;
                                                                                                                    Indels
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                                                                                                                   1217
                                                          272
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GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghu.

APPLICANT: Asundi, Vino

APPLICANT: Asundi, Vino

APPLICANT: Asundi, Vino

APPLICANT: Drmanac, Rad

TITLE OF INVENTION: NOVE.

TITLE OF INVENTION: POL:

FILE REFERENCE: 784CIP2Bil

CURRENT FILING DATE: 2000-(

PRIOR APPLICATION NUMBER

PRIOR FILING DATE: 2000-(

PRIOR FILING DATE: 2000-(

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE: 2000-(

NUMBER OF SEQ ID NOS: 111

SOFTWARE: PL-FL_genes Very

SEQ ID NO 707

LENGTH: 768

TYDE: DNA

ORGANISM: Homo Sapiens

PRAFURE: CDS

LOCATION: (109)...(486)

US-10-105-837-707
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US-10-105-837-707
Sequence 707, Application US/10105837
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                     SOFTWARE: pt_FL_genes Version
SEQ ID NO 707
LENGTH: 768
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                          Best Local Similarity Matches 272; Conserv
                                                                                                                                                                                                      Query Match
    221
                                252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Tang, Y. Tom
: Liu, Chenghua
: Asundi, Vinod
: Asundi, Vinod
: Zhao, Qing A.
: Dimanac, Radoje T
                 ACAAGGGTGAGAAGCAGCTGCCCGGTCCTGGACAAGACCAAGTTTTTTGGTCCCGGACCATG
                                                                        AGGAGGTACAGCAGATCCGCGACCAGCACCCCAGCAAAATCCCCGGTGATCATCGAGCGCT
                                                                                                                  CCCGCACCATGCCGTCGGAGAAGACCTTCAAGCAGCGCCGCCACCTTCGAACAAGAGTAG
                                                                                                                                             CCCGCGCGATGCCCTCAGACCGGCCTTTCAAGCAGCGGGGGAGCTTCGCCGACCGCTGTA 191
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                                                          AAGATGTCCGACTTATTCGAGAGCAGCATCCAACCAAAATCCCGGTGATAATAGAACGAT
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                                                                                                                                                                          Conservative
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74.1%;
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                                                                                                                                                                       Score 215; DB 6
Pred. No. 8e-44;
0; Mismatches
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US-10-286-897-1019
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Best Local :
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                                                      AAGATGTCCGACTTATTCGAGAGCAGCATCCAACCAAAATCCCGGTGATAATAGAACGAT
                                                                                                                              AGGAGGTACAGCAGATCCGCGACCAGCACCCCAGCAAAATCCCGGGTGATCATCGAGCGCT
TCAACATGAGTGAGCTCATCAAGATAATTAGAAGGCGCTTACAGCTCAATGCTAATCAGG
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(486)
US-10-286-897-1019
                                                                                                                                                                           NUMBER OF SEQ ID NOS: 714
SOFTWARE: pt FL_genes_b V
SEQ ID NO 1019
LENGTH: 768
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/09/552,317
PRIOR APPLICATION NUMBER: US/09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR PRIOR APPLICATION NUMBER: US/09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US/09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US/09/653,450
PRIOR APPLICATION NUMBER: US/09/653,450
PRIOR APPLICATION NUMBER: US/09/662,191
PRIOR APPLICATION NUMBER: US/09/662,191
PRIOR APPLICATION NUMBER: US/09/662,191
PRIOR APPLICATION NUMBER: US/09/662,191
PRIOR FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1019, Application US/10286897 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US/09/727,344
PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/286,897 CURRENT FILING DATE: 2002-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Novel Nucleic Acid and FILE REFERENCE: 784FLPCT
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  cch 33.6%; al Similarity 74.1%; 272; Conservative
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  0;
Score 215; DB 6
Pred. No. 8e-44;
0; Mismatches
                                            DB 6;
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95;
                                          Length 768
  Indels
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Gaps
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PRIOR APPLICATION NUMBER: US09/55,317
PRIOR APPLICATION NUMBER: US09/59,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR APPLICATION NUMBER: US09/65,191
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR APPLICATION NUMBER: US09/693,036
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US-10-258-898A-1019
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SEQ_ID_NO_1019
                                                                                                                                                                                                                                                                                                                                               Matches
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IITLE OF INVENTION: Novel Nucleic Acid and

FILE REFERENCE: 784FLPCT

CURRENT APPLICATION NUMBER: US/10/258,898A

CURRENT FILING DATE: 2002-10-29

CURRENT FILING DATE: 2002-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/488,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (10
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                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                              Similarity
               CCTTCTTCCTGCTGAACCAGCACAGCATGGTGACTGTTCCACGCCCATCGCGGACA 431
                                                                                       TCAACATGAGCGAGTTGGTCAAGATCATCCGGCGCCCCCCGCAGCTGAACCCCACGCAGG
                                                                                                                                                                                                       AAGATGTCCGACTTATTCGAGAGCAGCATCCAACCAAAATCCCGGTGATAATAGAACGAT
                                                                                                                                                                                                                                                                                          CCCGCGCGCATGCCCTCAGACCGGCCTTTCAAGCAGCGGCGGAGCTTCGCCGACCGCTGTA
CCTTCTTCCTGTTGGTGAACGGACACAGCATGGTCAGCGTCTCCACACCAATCTCAGAGG
                                                                                                                                   ACAAGGGTGAGAAGCAGCTTCCTGTTCTGGATAAAACAAAGTTCCTTGTACCTGACCATG
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                                                                 TCAACATGAGTGAGCTCATCAAGATAATTAGAAGGCGCTTACAGCTCAATGCTAATCAGG
                                                                                                                                                                   ACAAGGGTGAGAAGCAGCTGCCCGTCCTGGACAAGACCAAGTTTTTGGTCCCGGACCATG
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74.1%;
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Pred. No. 8e-44;
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Sequence 4591, Appli GENERAL INFORMATION:
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SEQ ID NO 4591
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PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US/09/727,344
PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/286,897 CURRENT FILING DATE: 2002-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US/
PRIOR FILING DATE: 2000-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/488,725 PRIOR FILING DATE: 2000-01-21
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NUMBER OF SEQ ID NOS: 7143
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PRIOR APPLICATION NUMBER: US/09/620,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/552,317
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CCTTCGG
                                          TGTATGAGAGTGAGAAGATGAAGATGGATTCCTGTACATGGTCTATGCCTCCCAJGAGA
                                                                                                                              CCTTCTTCCTGCTGGTGAACCAGCACAGCATGGTGAGTGTGTCCACGCCCATGGGGAACA 431
                                                                                                                                                                                                                                                 AGGAGGTACAGCAGATCCGCGACCAGCACCCCAGCAAAATCCCGGGTGATCATCGACCCT
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                                                                                      TCTACGAGCAGGAGAAAGACGAGGACGGCTTCCTCTATATGGTCTACGCCTCCCAGGAAA 491
                                                                                                                                                                                                                         TCAACATGAGTGAGCTCATCAAGAIAATTAGAAGGCGCTTACAGCTCAATGCTAATCAGG
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Pred. No. 1.1e-43;
0; Mismatches 95
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; Sequence 4591, <u>Application</u> US/10258898A
Sequence 2841, Application US/10293244 GENERAL INFORMATION: APPLICANT: Hyseq, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: pt_FL_genes_b
SEQ ID NO 4591
LENGTH: 2309
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APPLICANT: Hyseq In
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Best Local
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PRIOR APPLICATION NUMBER: US09/653,450
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FPLICATION NUMBER: US09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
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CURRENT APPLICATION NUMBER: US/10/258,898A
CURRENT FILING DATE: 2002-10-29
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TITLE OF INVENTION: Novel Nucleic Acid and
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                                                                                                                                    CGTTCGG 1859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGATGTCCGACTTATTCGAGAGCAGCATCCAACCAAAATCCCCGGTGATAATAGAACGAT
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Pred. No. 1.1e-43;
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US-09-654-936A-107; Sequence 107, App

Application

US/09654936A

GENERAL INFORMATION:

Tang, Y. Tom Liu, Chenghua

Tom

Asundi, Vinod Zhou, Ping

APPLICANT: APPLICANT:

zhang, Jie Ren, Feiyan Zhao, Qing A. Xue, Aidong J.

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

r: Wehrman, Tom T: Wang, Jian Rui T: Drmanac, Radoje T. INVENTION: Novel Nucleic Acids INVENTION: Polypeptides

TITLE

RESULT

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; TYPE: DNA
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SOFTWARE: CUSEC
SEQ ID NO 2841
FENCTH: 374
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
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CURRENT FILING DATE: 2002-11-12
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APPLICATION NUMBER: 09/654,936
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AAGGATGAGGATGGCTTCGTGTACATGACCTACGCCTCCCAGGAGACATTTGGCTGC
                                 AAAGACGAGGACGGCTTCCTCTATATGGTCTACGCCTCCCAGGAAACCTTCGGCTTC 502
                                                                      GTGAACAACAAGAGCCTGGTCAGCATGAGCGCAACCATGGCAGAGATCTACAGAGACTAC
                                                                                         GTGAACCAGCACAGCATGGTGAGTGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAG
                                                                                                                                          TTCCTCAGCATCATCCGGAGCCGCATGGTCCTGAGAGCCACGGAAGCCTTTTACTTGCTG
                                                                                                                                                            TTGGTCAAGATCATCCGGCGCCGCCTGCAGCCTGAACCCCACGCAGGCCTTCTTCCTGCTG
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Pred. No. 8e-
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US-10-293-244-873
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                                   PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-16
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/50,875
PRIOR APPLICATION NUMBER: 09/50,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
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SOFTWARE: pt_FL_genes Version 1.0
SEQ ID No 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides FILE REFERENCE: 21272-029
CURRENT APPLICATION NUMBER: US/10/293,244
CURRENT FILING DATE: 2002-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hyseq, Inc
APPLICANT: Tang, Y.
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CURRENT APPLICATION NUMBER: US/09/654,936A
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: Not Yet Assigned
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                         PRIOR FILING DATE: 2000-02-03
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LOCATION: (120)..(527)
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SEQ ID NOS: 3960
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; LOCATION: (120)..(527)
US-10-293-244-873
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                                                                                             SEQ ID NO 94
LENGTH: 535
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                                                                                                                                   SOFTWARE:
                                                                                                                                                      Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 353
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PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/236,557 PRIOR FILING DAIE: 1999-01-26
                                                                                                                                                                                          PRIOR FILING DATE: 1997-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/USV8/15949 PRIOR FILING DATE: 1998-07-29
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                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
NAME/KEY: SITE
LOCATION: (529)
                                      FEATURE
                                                                             TYPE: DNA
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                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/054,215 FILING DATE: 1997-07-30
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/054,236 FILING DATE: 1997-07-30
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-07-30
APPLICATION NUMBER: 60/054,218
FILING DATE: 1997-07-30
                                                                                                                                                                                                               APPLICATION NUMBER: 60/054,211
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                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1997-07-30
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/054,214
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RESULT 12
US-10-085-783A-26616
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US-10-626-717-7205
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US-09-820-649-94
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PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 10952
SEQ ID NO 7205
LENGTH: 448
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Best Local Similarity
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APPLICANT: De La Pena, Robert C.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 38-21(15978)D
CURRENT APPLICATION NUMBER: US/10/626,717
CURRENT FILING DATE: 2003-07-25
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                                                                                                                                             ACACTCTTCCACCGACAGCTGCCCTGATGTCTGCCATTTACGAGGAGAACAAGGACGAGG
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Pred. No. 2.9e-08;
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Pred. No. 2e-15;
2; Mismatches
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SEQ ID NO 26616
LENGTH: 469
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Best Local :
         PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR PLING DATE: 2001-02-28
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                                                                                                                                                APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing
FILE REFERENCE: 4231/2002
                                                                                                                    CURRENT APPLICATION NUMBER: US/10/085,783A CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 58994
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PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 4231/2002
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ORGANISM: Human
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SOFTWARE: PatentIn version 3.2 SEQ ID NO 10191

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US-10-085-783A-20079; Sequence 20079, Application US/10085783A
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEO ID NOS: 58994
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/085,783A CURRENT FILING DATE: 2002-02-28
                                                                                                                                                                                                                                                                                                                                APPLICANT: Liew, C.C. TITLE OF INVENTION: Compositions and Methods Relatiing to FILE REFERENCE: 4231/2002
                                                                                                                                                        SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ChondroGene Inc. APPLICANT: Liew, C.C.
            NAME/KEY: misc_feature LOCATION: (18)..(18) OTHER INFORMATION: n is a,
                                                                  FEATURE:
                                                                                    ORGANISM: Human
                                                                                                       TYPE: DNA
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FEATURE
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; GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-02-28
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. BM925959 AGENCOURT BM919877 AGENCOURT B1667032 603291206 BG715828 602675240 Description REFERENCE AUTHORS TITLE ACCESSION VERSION RESULT 1 BM925959 LOCUS COMMENT SOURCE KEYWORDS DEFINITION C JOURNAL ORGANISM 1149 bp mRNA linear EST 12-MAR-2002 AGENCOURT_6649827 NIH_MGC_114 Homo sapiens cDNA clone IMA/E:5764795 5', mRNA sequence. Eukaryota; Metazoa; Chordata; Ci Mammalia; Butheria; Primates; Ca 1 (bases 1 to 1149) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, N cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov http://dimage.llnl.gov m.column: 04 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. Homo sapiens EST High quality sequence start: 3 Unpublished Homo sapiens (human) BM925959.1 GI:19376434 ALIGNMENTS Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. Mammalian Gene Collection (MGC)

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/db_xref="taxon:9606"
/clone="IMAGE:5764395"
/lab_host="DH10B"
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99.7%;
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Pred. No. 6.7
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                       CCGACCGCTGTAAGGAGGTACAGCAGATCCGCGACCAGCACCCCAGCAAAATCCCGGTGA
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ACCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCACAGCATGGTGAGTGTGTCCACGC
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239

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CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Emammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1074)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
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LLAM12779 row: g
                                                                                                                                                                                                     /notee "Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 0.25. Note: this is a NIH_MGC Library." 308 c 369 g 137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5749663"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_120"
/note="Organ: pooled pan
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                                                                                                     Score 625.8; DB 12; Pred. No. 1.4e-119;
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Matches 606; Conserv
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Plate: LLAM11787 row: k column:
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sl
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 700)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian G
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BI667032.1 GI:15581265
                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 694.
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                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                              a
                                                                                                                                                                                               /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sali-xhoI (gtcgag pBluescript KS+); Site_1: Formal primer 5'-TTTITTTTTTTTVN-3', Size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched
                                                                                                            Institutes of Health). Note: this is a NIH_MGC _{1} 235 _{2} 223 _{3} 113 _{4}
                                                                                                                                            for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Li constructed by M. Brownstein (NIMH/NHGRI, National
                                                                                                                                                                                                                                                                                                              /clone="IMAGE:5310840"
/tissue_type="hypothalamus"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
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98.1%;
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                    0;
                   Score 598.8; DB 12
Pred. No. 5.1e-114;
0; Mismatches 12;
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           Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGKI), a CDNA Library Preparation: Michael J. Brownstein (NHGKI), a Toshiyuki and Piero Carcinci (KHKEN) CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genemics, Inc. Clone distribution: MGC clone distribution information can found through the L.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                     705 bp mRNA linear ESI 08:M. 602675240F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4797945 mRNA sequence. BG715828 BG715828.1 GI:13995015 ESI.
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/lab_host="DH10B"
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/clone="IMAGE:4797945"
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/mol_type="mRNA"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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BM919896
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Plate: LLAM12779 row: h column: 08
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National Institutes of Health, Mammalian
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                                                              CATCCGGCGCCGCCTGCAGCTGAACCCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCA 396
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/note="organ: pooled pancreas and spleen; Vector:
note="organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

a 291 c 399 g 185 t 92 others
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/mol_type="mrNA"
/db_xref="taxon:9606"
/clone="IMAGE:5749687"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information ca found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1115)
NIH-MGC http://mqc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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BM924606
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AGENCOURT_6767666 NIH_MGC_116 Homo
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Plate: LLAM12808 row: o column:
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                                 Conservative
                                                                                                                /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcokV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
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/clone="IMAGE:5760990"
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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                                                                                                                                                  Email: cgapbs-rimail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHHH), i
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The L.M.A.G.E. Consortion (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                           Unpublished Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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BI824755
603033636F1 NIH_MGC_115 i
mRNA sequence.
BI824755
BI824755.1 GI:15936305
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                                                                                                                                                                                                                                                                                               CCAGCAGTAGGGGGGCTCGGCCTGGGAGTCGGGGGGCCCCGGTCAGGCCCCTGCCCAGAGA
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/clone_lib="NH_MGC_96"
/clone="NH_MGC_96"
/clone="NH_MGC_96"
/clone="NH_MGC_1"
/clone="
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Pred. No. 7.2e-111;
0; Mismatches 4;
                                                                Homo
                                                              bp mRNA linear EST 04-OCT-2001 sapiens cDNA clone IMAGE:5174817 5',
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                                  TGAGTGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAGAAGAAGACGAGGACGACTTCC
                                                                                                                       GCCGCCTGCAGCTGAACCCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCACAGCATGG
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                                                                                                                                                                                                                                                                 GCAAAATCCCGGTGATCATCGAGCGCTACAAGGGTGAGAAGCAGCTGCCCGTCCTGGACA
                                                                                                                                                                                                                                                                                         GCAAAATCCCGGTGATCATCGAGCGCTACAAGGGTGAGAAGCAGCTGCCCGTCCTGGACA
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               TGAGTGTCCACGCCCATCGCGACATCTACGAGCAGGAGAAAGACGAGGACGGCTTCC
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0;

Mismatches

Indels

1;

Gaps

420 464 404

360

240

344

300

180

224

284

164

60 104

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High quality sequence stop: Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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                                                                                                   /note-"Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
oligo-dT promed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb: Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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/clone="IMAGE:5174817"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo
91.0%;
Score 582.4; DB 12; Pred. No. 1.3e-110;
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                        Length 738;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGENCOURT_6767682 NIH_MGC_116 Hc 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bloscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                           Similarity
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                                     AGCCGGGCCGCGCGATGCCCTCAGACCGGCCTTTCAAGCAGCGGCGGAGCTTCGCCGAC
                                                                                                                      CCCCGGAGCCCCAAACCGCAGACACATCCCCGCGCCCCAGAGCCCCGGCCTGCGCCCC 124
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                                                                              CCCCGGAGCCCCCAAACCGCAGACACATCCCCGCGCCCCAGAGCCCCGGCCTGCGCGCCC
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           quality sequence start: 44 quality sequence stop: 718
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//db_xre!="txxn:9606"
//db_xre!="txxn:9606"
//db_xre!="txxn:9606"
//lab_host="f0H10B"
//lab_host="f0H10B"
//clone_lib="NHH_MCC_116"
//clone_lib="NHH_MCC_116"
//note="organ: pooled colon, kidney, stomach: Vector:
pcMV-SpORT6; Site_l: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
190 a 317 c 409 g 196 t 39 others
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                           90.0%;
99.8%;
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                                                                                                                                                                                           Score 575.8; DB 12
Pred. No. 3.1e-109;
                                                                                                                                                                      Mismatches
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NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health.
                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs=r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa; Chordata; Graniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Plate: LLAM11605 row: c column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/clone_lib*_NHH_MGP_12]"
/clone_lib*_NHH_MGP_12]"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: EcoRV (destroyed); RNA source anonymous pool of
fetal brains, female age 20 weeks, female age 24 weeks,
                                                                                                   /lab_host="DH10B"
                                                                                                                   /organism="Homo sapiets"
/mol_type="mkNA"
/db_xref="taxon:9606"
/clone="IMAGE:5240007"
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                                                               Homo sapiens (human)
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      http://mgc.nci.nih.gov/
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                                 CTGAACCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAGCACAGCATGGTGAGTGTGTCC
           CGGGGGGCCCCGGTCAGGCCCTGCCCAGAGAGCTTCTGGTTCCTGAACTGAGCTGCCTCT
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High quality sequence stop: 671.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: LLAM11607
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    Conservative
                                                                                                                                      Site_2: ECGRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcGRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note
                                                                                                        this is
a 223
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapie
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D
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                              GACCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGGCGCCGCCTGCAGCTGAACCCC
                                                                                            GAGCGCTACAAGGGTGAGAAGCAGCTGCCCGGTCCTGGACAAGACCAAGTTIITGGTCCCG
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                                                                                                                                                                                                                 AGCCGGGCCGCGCGCGCTCAGACCGGCCTTTCAAGCAGCGGCGGAGCTTCGCCGAC 184
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Tissue Procurement: Lite Technologies, Inc
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/cote="Organ: brain: Not possible results and 24 weeks."
                                                                                                                                                                                                                                                            fetal brains, female age 20 weeks, female age 24 weeks and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon
                                                                                                                                             this
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Pred. No. 1.4e-100;
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                                                                                 Korea Research Institute of 52 Eoeun-dong Yuseong-gu, Da Tel: +82-42-860-4470
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Contact: Kim YS
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Kim, N.S., Hahn, Y.,
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                               quality sequence stop:
Location/Qualifiers
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                                                   yongsung@mail.kribb.re.kr
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   /organism="Homo sapiens"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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 GGGGGCCCC
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Search completed: August 15, 2003, 09:30:40 Job time: 2046 secs

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Run on:
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Maximum DB seq length: 2000000000
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    August 15, 2003, 08:56:30; Search time 249 Seconds (without alignments) 5752.136 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Query Match Length DB		ID	Description
1	640	100.0	640	1	US-09-904-603-2	Sequence 2, Appli
2	255.2	39.9	570	9	US-09-864-761-12594	Sequence 12594, A
w	238.6	37.3	861	10	US-09-917-800A-1714	Sequence 1714, Ap
4.	238.5	37.3	861	12	US-10-205-194-72	Sequence 72. Appl
ران ا	218.8	34.2	497	1	US-09-918-995-1874	Sequence 1874, Ap
6	215	33.6	768	14	US-10-037-270-707	Sequence 707, App
7	215	33.6	2250	9	US-09-925-301-209	Sequence 209, App
8	214.4	33.5	2199	14	US-10-277-156-3	Sequence 3, Appli
9 9	192.4	30.1	537	10	US-09-917-800A-1201	Sequence 1201, Ap
10	163	25.5	163	ç	US-09-864-761-28415	Sequence 28415, A
11	108.4	16.9	201	14	US-10-277-156-1	Sequence 1, Appli
c 12	95.6	14.9	474	9	US-09-864-761-885	Sequence 885, App
c 13	71.4	11.2	155	9	US-09-864-761-17665	Sequence 17665, A
14	71.4	11.2	975	10	US-09-917-800A-1711	Sequence 1711, Ap
15	71.4	11.2	975	14	US-10-205-342-24	Sequence 24, Appl
16	58.8	9.2	500	_	08-09-918-995-1734	CONTROL 1704

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7.1	7.1	7.1	7.1	7.2	7.2	7.2	7.3	7.3	7.3	7.3	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.7	7.7	7.8	7.9	7.9	7.9	7.5	8.5	8.9	, ,
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US-10-156-761-1	US-10-156-761-5751	US-09-910-664-59	US-09-918-995-6964	US-09-814-122-16	us-10-027-632-276666	us-10-156-761-6762	US-10-027-632-9167	US-10-027-632-9166	US-10-027-632-9165	US-10-156-761-4852	US-10-017-754-78	US-09-476-300-78	US-09-849-626-78	US-09-902-941-78	US-09-736-457-78	us-10-171-581-105	US-09-919-580-198	US-09-918-995-28426	US-10-037-270-597	US-09-919-580-825	US-10-205-194-161	US-10-156-761-1	08-10-156-761-2959	US-10-091-504-2109	US-09-764-869-2109	US-09-770-149-663	US-09-938-842A-461	CC 10 010 001 110000
Sequence 1, Appli	Sequence 5751, Ap	Sequence 59, Appl	Sequence 5964, Ap	Sequence 16, Appl	Sequence 276466,	Sequence £762, Ap	Sequence 9167, Ap	Sequence 9166, Ap	Sequence 9165, Ap	4857			78,		Sequence 78, Appl	Sequence 105, App	Sequence 198, App	Sequence 28426, A	Sequence 597, App	Sequence 825, App	Sequence 161, App	Sequence 1. Арр1	Sequence 2959, Ap	Sequence 2169, Ap	Sequence 2199, Ap	Sequence 663, App	Sequence 461, App	Suduante Thousan

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RESULT 1
US-09-904-603-2
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; Publication No. US20030099612A1
; GENERAL INFORMATION:
                                      TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                               TELEPAX: 415-845-4166
                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: 08/805,117
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/904,603
FILING DATE: 12-Jul -2001
CLASSIFICATION: «Unknown»
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TITLE OF INVENTION: NOVEL MICRETUBULE: ASSOCIATED PROTEIN NUMBER OF SECUENCES: 3
                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: Dos
                                                                                                                                                                                                                             FILING DATE: <Unknown
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
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STREET: 3174 Porter Drive
LENGTH: 640 base pairs
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US-09-864-761-12594
; Sequence 12594, Application
; Patent No. US20020048763A1
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Best 1
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-x-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312
                                                                               APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
Local Similarity
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Pred. No. 7.6e-157;
Mismatches 0;
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CORGANISM: Homo sapie
FEATURE:
OTHER INFORMATION: M
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RAPPLICATION NUMBER: PCT/US01/00665

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00668

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00663

OR APPLICATION NUMBER: PCT/US01/00663

OR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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            GAACTGAGCTGCCTCTACCG
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                                                                  GGCTCGGCCTGGGAGTCGGGCGGCCCCGGTCAGGCCCTGCCCAGAGAGCTCCTGGTTCCT
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PRIOR FILING DATE: 2000-07-71
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/298,884
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NUMBER OF SEQ ID NOS: 1740
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                                      GCCCATCGCGGACATCTACGAGCAGGAGGAGGACGAGGACGGCTTCCTCTATATGGTCTA
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76.68;
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APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
                                                                                          Sequence 1874, Application US/09918995 Publication No. US20030073623A1
                                                                      GENERAL INFORMATION:
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Best Local Similarity
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PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 177
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CURRENT FILING DATE: 5200-07-24
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             APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CONA LIBRARIES
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TITLE OF INVENTION: Identification and Use
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REFERENCE:
                                                                                                                                                                                                                                             478 CGCCTCCCAGGAAACCTTCGG 498
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                                                                                                                                                                                                                                                                                                        418 GCCCATCGCGGACATCTACGAGCAGGAGAAAJACGAGGACGGCTTCCTCTATATGTTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 CGCCTCCCAGGAAACCTTCGG
                                                                                                                                                                                                                                                                                                                                                             245 CAATGCTAACCAAGCCTTCTTCC1CCTGGTGAATGGGCACAGCATGGTGAGTGTGTCCAC
                                                                                                                                                                                                                                                                                                                                                                             358 GAACCCCACGAGGCCTTCTTCCTGCTGGTGAACCAGCACAGCATGGTGAGTGTGCTCAC
                                                                                                                                                                                                          365 TGCCICCCAGGAGACGTTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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76.6%;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Molecules Implicated
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RESULT 6
US-10-037-270-707
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                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                  Publication No.
                                                                                                                                                                                                                                 Sequence 707,
                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1874
                                                                      APPLICANT:
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                                APPLICANT:
                                            APPLICANT:
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                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CENGTH:
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                                                                                                                                                                                                                                                                                           GATGGATTCCTGTACATGGTCTATGCCTCCCAGGAGACGTTCGG
Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
                                                                                                                                  Asundi, Vinod
Zhang, Jie
Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                               CACAGCATGGTCAGCGTCTCCACACCAATCTCAGAGGTGTATGAGAGTGAGAAAGATGAA
                                                                                                                                                                                                                                                                                                                                                                       CACAGCATGGTGAGTGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAGAAAGACGAG 454
                                                                                                                                                                                                                                                                                                                                                                                                   ATAATTAGAAGGCGCTTACAGCTCAATGCTAATCAGGCCTTCTTCCTGTTGGTGAACGGA 372
                                                                                                                                                                                                                                                                                                                                                                                                                    ATCATCCGGCGCCCTGCAGCTGAACCCCACGCAGGCCTTCTTCCTGCTGGTGAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTTCAAGCAGCGCCGCACCTTCGAACAAAGAGTAGAAGATGTCCGACTTATTCGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTTTCAAGCAGCGGCGGAGCTTCGCCGACCGCTGTAAGGAGGTACAGCAGATCCGCGAC 214
                                     Zhou,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCCTGGACAAGACCAAGTTTTTGGTCCCGGACCATGTCAACATGAGCGAGTTGGTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGCATCCAACCAAAATCCCCGGTGATAATAGAACGATACAAGGGTGAGAAGCAGCTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGACCCTCGCGTCGACGCCGCCGCCGCCCAGATCCCCGCACCATGCCGTCGGAGAAG
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                                                                 Xue, Aidong J.
Yang, Yonghong
                                                                                            Wehrman, Tom
                                                                                                         Zhao, Qing A.
                                                                                                                     Chen, Rui-hong
                                                        Wang,
                                                                                                                                                                              Liu,
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66.8%;
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RESULT 7 US-09-925-301-209

Sequence 209, Application US/09925301
Patent NO. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10

SOFTWARE:

PatentIn Ver. 2.0

10 ID NO 209 LENGTH: 2250 CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694

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; LOCATION: (109)..(486)
US-10-037-270-707
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
-- Local Similarity
-- Conserv
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SEQ ID NO 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 768
TYPE: DNA
ORGANISM: Homo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. US20030104529Alel Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 1104
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PRIOR FILING DATE: 2000-04-25
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                            492 CCTTCGG 498
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                                                                                                                                                                                                                                                                                               192 AGGAGGTACAGCAGATCCGCGACCAGCACCCCAGCAAAATCCCCGGTGATCATCGAGCGCT 251
                                                                                                                                                                                                                                                                                                                                               101
                                                  TGTATGAGAGTGAGAAGATGAAGATGCTGTACATGGTCTATGCCTCCCAGGAGA
                                                                TCTACGAGCAGGAGAAAGACGACGACGACGTTCCTCTATATGGTCTACGCCTCCCAGGAAA 491
                                                                                                          CTTCTTCTTTGGTGAACGGACACAGCATGGTCAGCGTCTCCACACCAATCTCAGAGG
                                                                                                                          CCTTCTTCCTGCTGGTGAACCAGCACAGCATGGTGAGTGTGTCCACGCCCATCGCGGACA 431
                                                                                                                                                                TCAACATGAGTGAGCTCATCAAGATAATTAGAAGGCGCTTACAGCTCAATGCTAATCAGG
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                                                                                                                                                                                   TCAACATGAGCGAGTTGGTCAAGATCATCCGGCGCCGCCTGCAGGTTGAACCCCCACGCAGG
                                                                                                                                                                                                                       ACAAGGGTGAGAAGCAGCTGCCCGTCCTGGACAAGACCAAGTTTTTGGTCCCGGACCATG
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74.1%;
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Pred. No. 1.6e-46;
D; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 768;
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: TYPE: DNA
; ORGANISM: Human
US-10-277-156-3
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US-10-277-156-3
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Best Local :
                                                                                              Query Match
Best Local 8
                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 272; Conserv
                                                                                 Matches
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/277,156
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 09/708,725
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/243,428
PRIOR APPLICATION NUMBER: 60/243,428
PRIOR FILING DATE: 2000-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LADUNGA et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL000842 DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: (23)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n equals a,t,g, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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    750
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                                                                                                Similarity
                      CCGGAGCCCCAAACCGCAGACACATCCCCCGCGCCCAGAGCCCCGGCCTGCGCCCAG
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CCGCAGCAGCCGCCACCCCAGGAGCCGCCGGGACCCTCGCGTCGTCGCCGCCGCCGCCCC 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCGCGCGATGCCCTCAGACCGGCCTTTCAAGCAGCGGCGGAGCTTCGCCGACCGCTGTA 191
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68.5%;
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74.1%;
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                                                                           Score 214.4; DB 14; Length 2199; Pred. No. 2.5e-46; 0; Mismatches 136; Indels 0;
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Pred. No. 1.7e-46;
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RESULT 9
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; OTHER INFORMATION: Genbank Accession No. US-09-917-800A-1201
                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: U
PRIOR FILING DATE: 2001-05-
PRIOR APPLICATION NUMBER: U
PRIOR FILING DATE: 2001-05-
PRIOR APPLICATION NUMBER: U
PRIOR FILING DATE: 2001-66-
PRIOR APPLICATION NUMBER: U
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                                                                                         SOFTWARE: Patentin
SEQ ID NO 1201
LENGTH: 537
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                                                                                                                                   NUMBER OF SEQ ID NOS: 1740 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-11-02 PRIOR APPLICATION NUMBER: US 6 PRIOR FILING DATE: 2001-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/917,800A CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Molecular Toxicology Modeling FILE REFERENCE: 44921-5038-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-07-31 PRIOR APPLICATION NUMBER: US 60/222,880
                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 50/222,040
                                                     ORGANISM: Rattus norvegious
                                       FEATURE:
                                                                             TYPE: DNA
                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 6 FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 6 FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/290,029 FILING DATE: 2001-05-11
                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/298,884
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/297,457
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Gene Logic, Inc.
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Castle, Arthur
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Query Match

30.1%;

Score 192.4;

DB 10;

Length 537:

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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-92
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28415, Application US/09864761 Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                        APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 2001-01-30
                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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0; Mismatches 56;
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; ORGANISM: Human
US-10-277-156-1
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.66

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.66

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.65

OTHER INFORMATION: NT HIT: U05784.1, EVALUE 5.00e-16

OTHER INFORMATION: EXT HUMAN HIT: BE712961.1, EVALUE 7.00e-
OTHER INFORMATION: SWISSPROT HIT: Q62625, EVALUE 4.00e-20

US-09-864-761-28415
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Best Local Sin
Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version SEQ ID NO \mathbf{1}
                                                                                                                                                                                                                                             Matches
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence I
SEQ ID NO 28415
LENGTH: 163
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APPLICANT: LADUNGA et al.

TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REFÉRENCE: CL000842 DIV

CURRENT APPLICATION NUMBER: US/10/277,156

CURRENT FILING DATE: 2002-10-22

CURRENT FILING DATE: 2002-10-27
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                                             TTCCTGTTGGTGAACGGACACAGCATGGTCAGCGTCTCCACACCAATCTCAGAGGTGTAT
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REILING DATE: 2000-02-04
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APPLICATION NUMBER: PCT/US01/00668
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65.48;
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Pred. No. 1.5e-1
0; Mismatches
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Sequence 1711, Application US/09917800A; Patent No. US20020119462A1; GENERAL INFORMATION:
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                                                                    CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/295,798
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                                                                                                                                                                                                                                                                                        APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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PRIOR APPLICATION NUMBER: US 0
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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ORGANISM: Homo sapiens
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Castle, Arthur
Elashoff, Michael
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N: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

N: EXPRESSED IN HELA, SIGNAL = 2.1

N: EXPRESSED IN HEARIN, SIGNAL = 1.5

N: EXPRESSED IN HEARIN, SIGNAL = 1.5

N: EXPRESSED IN PLACENTA, SIGNAL = 0.9

N: EXPRESSED IN PLAT4, SIGNAL = 0.93

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

N: EXPRESSED IN LUNG, SIGNAL = 1.5

N: EXPRESSED IN HELLOO, SIGNAL = 1.5

N: EXPRESSED IN HELLOO, SIGNAL = 1.3

N: NIT HIT: U80885.1, EVALUE 2.00e-10

ON: EST_HUMAN HIT: AA723823.1, EVALUE 3.00e-72
  NUMBER:
                                2001-06-06
NUMBER: US 60/297,457
                    2001-06-13
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Pred. No. 2.7e-09;
0; Mismatches 51
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; OTHER INFORMATION: cDNA: Ganglioside expression US-10-205-342-24
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US-10-205-342-24
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NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1711
LENGTH: 975
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_022706 US-09-917-800A-1711
                                                SEQ ID NO 24
LENGTH: 975
TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/10205342 Publication No. US20030108906A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                           APPLICANT: Pinnock, Robert TITLE OF INVENTION: Identification and Use FILE REFERENCE: WL-A-018198 CURRENT APPLICATION NUMBER: US/10/205,342 CURRENT FILING DATE: 2002-07-24
                                                                                                                                                                                                                                                                                                 APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
APPLICANT: Dixon, Alistair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 215;
                                                                                                                                     PRIOR APPLICATION NUMBER: GB 0118354.0 PRIOR FILING DATE: 2001-07-27 NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                        SOFTWARE:
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PRIOR APPLICATION NUMBER: US
                                   FEATURE:
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                                                                                                                        PatentIn version
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                                                                                                                                                                                                                                                                                Brooksbank, Robert
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Search completed: August 15, 2003, 10:34:15 Job time : 259 secs
                                                                          В
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                                                                  350 AAGACAGTCCCACAGTCCAGCCTAACT---ATGGCACAGCTTTACGAGAAGGAAAAAAAA 406
                                                                                                                                                                     392 CAGCACAGCATGGTGAGTGTGTCCACGCCCATCGCGGACATCTACGAGCAGGAGAAAGAC 451
                                                                                                                                                                                                                    290 TGGATCATCAGGAAAAGGATCCAGCTTCCTTCTGAGAAGGCCATCTTCTTGTTGTGGAC 349
                                                                                                                                                                                                                                          332 AAGATCATCCGGCGCCGCCTGCAGCTGAACCCCCACGCAGGCCTTCTTCCTGCTGGTGAAC 391
                                                                                                                                                                                                                                                                                                 230 GTTGACATTGACAAGAGGAAGTACTTGGTCCCATCTGACATCACTGTGGCTCAGTTCATG 289
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                                                                                                                                                                                                                                                                                                                                                                           173 GCGAAATACCCCGACCGGGTTCCGGTGATCGTTGAG---AAAGTCTCTGGCTCTCAGATT 229
                                                                                                                                                                                                                                                                                                                                                                                                 212 GACCAGCAGCAGCAAAATCCCGGTGATCATCGAGCGCTACAAGGGTGAGAAGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 TGGATGTTTAAGGAGGACCACTCGCTGGAACACAGATGCGTGGAATCCGCGAAGATCAGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 CGGCCTTTCAAGCAGCGGCGGAGCTTCGCCGACCGCTGTAAGGAGGTACAGCAGATCCGC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 TOGETTEGECGAAGTETGEGGETCAAAGAGECGGETECGTEGETTECCGGCGCCATGAAG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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